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(54) Title: MAMMALIAN GENES INVOLVED IN VIRAL INFECTION AND TUMOR SUPPRESSION

(57) Abstract

The present invention provides methods of identifying cellular genes necessary for viral growth and cellular genes that function as tumor suppressors. Thus, the present invention provides nucleic acids related to and methods of reducing or preventing viral infection or cancer. The invention also provides methods of producing substantially virus-free cell cultures and methods for screening for additional such genes.

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MAMMALIAN GENES INVOLVED IN VIRAL INFECTION AND TUMOR SUPPRESSION

BACKGROUND

Field of the Invention

The present invention provides methods of identifying cellular genes used for viral growth or for tumor progression. Thus, the present invention relates to nucleic acids related to and methods of reducing or preventing viral infection and for suppressing tumor progression. The invention also relates to methods for screening for additional such genes.

Background art

Various projects have been directed toward isolating and sequencing the genome of various animals, notably the human. However, most methodologies provide nucleotide sequences for which no function is linked or even suggested, thus limiting the immediate usefulness of such data.

The present invention, in contrast, provides methods of screening only for nucleic acids that are involved in a specific process, *i.e.*, viral infection or tumor progression, and further, for nucleic acids useful in treatments for these processes because by this method only nucleic acids which are also nonessential to the cell are isolated. Such methods are highly useful, since they ascribe a function to each isolated gene, and thus the isolated nucleic acids can immediately be utilized in various specific methods and procedures.

For, example, the present invention provides methods of isolating nucleic acids encoding gene products used for viral infection, but nonessential to the cell. Viral infections of the intestine and liver are significant causes of human morbidity and mortality. Understanding the molecular mechanisms of such infections will lead to new approaches in their treatment and control.

Viruses can establish a variety of types of infection. These infections can be generally classified as lytic or persistent, though some lytic infections are considered persistent. Generally, persistent infections fall into two categories: (1) chronic (productive) infection, *i.e.*, infection wherein infectious virus is present and can be

recovered by traditional biological methods and (2) latent infection, *i.e.*, infection wherein viral genome is present in the cell but infectious virus is generally not produced except during intermittent episodes of reactivation. Persistence generally involves stages of both productive and latent infection.

Lytic infections can also persist under conditions where only a small fraction of the total cells are infected (smoldering (cycling) infection). The few infected cells release virus and are killed, but the progeny virus again only infect a small number of the total cells. Examples of such smoldering infections include the persistence of lactic dehydrogenase virus in mice (Mahy, B.W.J., *Br. Med. Bull.* 41: 50-55 (1985)) and adenovirus infection in humans (Porter, D.D. pp. 784-790 in Baron, S., ed. *Medical Microbiology* 2d ed. (Addison-Wesley, Menlo Park, CA 1985)).

Furthermore, a virus may be lytic for some cell types but not for others. For example, evidence suggests that human immunodeficiency virus (HIV) is more lytic for T cells than for monocytes/macrophages, and therefore can result in a productive infection of T cells that can result in cell death, whereas HIV-infected mononuclear phagocytes may produce virus for considerable periods of time without cell lysis. (Klatzmann, et al. *Science* 225:59-62 (1984); Koyanagi, et al. *Science* 241:1673-1675 (1988); Sattentau, et al. *Cell* 52:631-633 (1988)).

Traditional treatments for viral infection include pharmaceuticals aimed at specific virus derived proteins, such as HIV protease or reverse transcriptase, or recombinant (cloned) immune modulators (host derived), such as the interferons. However, the current methods have several limitations and drawbacks which include high rates of viral mutations which render anti-viral pharmaceuticals ineffective. For immune modulators, limited effectiveness, limiting side effects, a lack of specificity all limit the general applicability of these agents. Also the rate of success with current antivirals and immune-modulators has been disappointing.

The current invention focuses on isolating genes that are not essential for cellular survival when disrupted in one or both alleles, but which are required for virus replication. This may occur with a dose effect, in which one allele knock-out may confer the phenotype of virus resistance for the cell. As targets for therapeutic intervention, inhibition of these cellular gene products, including: proteins, parts of

proteins (modification enzymes that include, but are not restricted to glycosylation, lipid modifiers [myriolate, etc.]), lipids, transcription elements and RNA regulatory molecules, may be less likely to have profound toxic side effects and virus mutation is less likely to overcome the 'block' to replicate successfully.

The present invention provides a significant improvement over previous methods of attempted therapeutic intervention against viral infection by addressing the cellular genes required by the virus for growth. Therefore, the present invention also provides an innovative therapeutic approach to intervention in viral infection by providing methods to treat viruses by inhibiting the cellular genes necessary for viral infection. Because these genes, by virtue of the means by which they are originally detected, are nonessential to the cell's survival, these treatment methods can be used in a subject without serious detrimental effects to the subject, as has been found with previous methods. The present invention also provides the surprising discovery that virally infected cells are dependent upon a factor in serum to survive. Therefore, the present invention also provides a method for treating viral infection by inhibiting this serum survival factor. Finally, these discoveries also provide a novel method for removing virally infected cells from a cell culture by removing, inhibiting or disrupting this serum survival factor in the culture so that non-infected cells selectively survive.

The selection of tumor suppressor gene(s) has become an important area in the discovery of new target for therapeutic intervention of cancer. Since the discovery that cells are restricted from promiscuous entry into the cell cycle by specific genes that are capable of suppressing a 'transformed' phenotype, considerable time has been invested in the discovery of such genes. Some of these genes include the gene associated by rhabdomyosarcoma (Rb) and the p53 (apoptosis related) encoding gene. The present invention provides a method, using gene-trapping, to select cell lines that have transformed phenotype from cells that are not transformed and to isolate from these cells a gene that can suppress a malignant phenotype. Thus, by the nature of the isolation process, a function is associated with the isolated genes. The capacity to select quickly tumor suppressor genes can provide unique targets in the process of treating or preventing, and even for diagnostic testing of, cancer.

DETAILED DESCRIPTION OF THE INVENTION

The present invention utilizes a "gene trap" method along with a selection process to identify and isolate nucleic acids from genes associated with a particular function. Specifically, it provides a means of isolating cellular genes necessary for viral infection but not essential for the cell's survival, and it provides a means of isolating cellular genes that suppress tumor progression.

The present invention also provides a core discovery that virally infected cells become dependent upon at least one factor present in serum for survival, whereas non-infected cells do not exhibit this dependence. This core discovery has been utilized in the present invention in several ways. First, inhibition of the "serum survival factor" can be utilized to eradicate persistently virally infected cells from populations of non-infected cells. Inhibition of this factor can also be used to treat virus infection in a subject, as further described herein. Additionally, inhibition of or withdrawal of the serum survival factor in tissue culture allows for the detection of cellular genes required for viral replication yet nonessential for an uninfected cell to survive. The present invention further provides several such cellular genes, as well as methods of treating viral infections by inhibiting the functioning of such genes.

Furthermore, the present invention provides a method for isolation of cellular genes utilized in tumor progression.

The present method provides several cellular genes that are necessary for viral growth in the cell but are not essential for the cell to survive. These genes are important for lytic and persistent infection by viruses. These genes were isolated by generating gene trap libraries by infecting cells with a retrovirus gene trap vector, selecting for cells in which a gene trap event occurred (*i.e.*, in which the vector had inserted such that the promoterless marker gene was inserted such that a cellular promoter promotes transcription of the marker gene, *i.e.*, inserted into a functioning gene), starving the cells of serum, infecting the selected cells with the virus of choice while continuing serum starvation, and adding back serum to allow visible colonies to develop, which colonies were cloned by limiting dilution. Genes into which the retrovirus gene trap vector inserted were then isolated from the colonies using probes specific for the retrovirus

gene trap vector. Thus nucleic acids isolated by this method are isolated portions of genes.

Thus the present invention provides a method of identifying a cellular gene necessary for viral growth in a cell and nonessential for cellular survival, comprising (a) transferring into a cell culture growing in serum-containing medium a vector encoding a selective marker gene lacking a functional promoter, (b) selecting cells expressing the marker gene, (c) removing serum from the culture medium, (d) infecting the cell culture with the virus, and (e) isolating from the surviving cells a cellular gene within which the marker gene is inserted, thereby identifying a gene necessary for viral growth in a cell and nonessential for cellular survival. The present invention also provides a method of identifying a cellular gene used for viral growth in a cell and nonessential for cellular survival, comprising (a) transferring into a cell culture growing in serum-containing medium a vector encoding a selective marker gene lacking a functional promoter, (b) selecting cells expressing the marker gene, (c) removing serum from the culture medium, (d) infecting the cell culture with the virus, and (e) isolating from the surviving cells a cellular gene within which the marker gene is inserted, thereby identifying a gene necessary for viral growth in a cell and nonessential for cellular survival. In any selected cell type, such as Chinese hamster ovary cells, one can readily determine if serum starvation is required for selection. If it is not, serum starvation may be eliminated from the steps.

Alternatively, instead of removing serum from the culture medium, a serum factor required by the virus for growth can be inhibited, such as by the administration of an antibody that specifically binds that factor. Furthermore, if it is believed that there are no persistently infected cells in the culture, the serum starvation step can be eliminated and the cells grown in usual medium for the cell type. If serum starvation is used, it can be continued for a time after the culture is infected with the virus. Serum can then be added back to the culture. If some other method is used to inactivate the factor, it can be discontinued, inactivated or removed (such as removing the anti-factor antibody, *e.g.*, with a bound antibody directed against that antibody) prior to adding fresh serum back to the culture. Cells that survive are mutants having an inactivating insertion in a gene necessary for growth of the virus. The genes having the insertions

can then be isolated by isolating sequences having the marker gene sequences. This mutational process disturbs a wild type function. A mutant gene may produce at a lower level a normal product, it may produce a normal product not normally found in these cells, it may cause the overproduction of a normal product, it may produce an altered product that has some functions but not others, or it may completely disrupt a gene function. Additionally, the mutation may disrupt an RNA that has a function but is never translated into a protein. For example, the alpha-tropomyosin gene has a 3' RNA that is very important in cell regulation but never is translated into protein. (*Cell* 75 pg 1107-1117 , 12/17/93).

As used herein, a cellular gene "nonessential for cellular survival" means a gene for which disruption of one or both alleles results in a cell viable for at least a period of time which allows viral replication to be inhibited for preventative or therapeutic uses or use in research. A gene "necessary for viral growth" means the gene product, either protein or RNA, secreted or not, is necessary, either directly or indirectly in some way for the virus to grow, and therefore, in the absence of that gene product (*i.e.*, a functionally available gene product), at least some of the cells containing the virus die. For example, such genes can encode cell cycle regulatory proteins, proteins affecting the vacuolar hydrogen pump, or proteins involved in protein folding and protein modification, including but not limited to: phosphorylation, methylation, glycosylation, myrislation or other lipid moiety, or protein processing via enzymatic processing. Some examples of such genes are exemplified herein, wherein some of the isolated nucleic acids correspond to genes such as vacuolar H+ATPase, alpha tropomyosin, gas5 gene, ras complex, N-acetyl-glucosaminyltransferase I mRNA, and calcyclin.

Any virus capable of infecting the cell can be used for this method. Virus can be selected based upon the particular infection desired to study. However, it is contemplated by the present invention that many viruses will be dependent upon the same cellular genes for survival; thus a cellular gene isolated using one virus can be used as a target for therapy for other viruses as well. Any cellular gene can be tested for relevancy to any desired virus using the methods set forth herein, *i.e.*, in general, by inhibiting the gene or its gene product in a cell and determining if the desired virus can grow in that cell. Some examples of viruses include HIV (including HIV-1 and HIV-2);

parvovirus; papillomaviruses; hantaviruses; influenza viruses (*e.g.*, influenza A, B and C viruses); hepatitis viruses A to G; caliciviruses; astroviruses; rotaviruses; coronaviruses, such as human respiratory coronavirus; picornaviruses, such as human rhinovirus and enterovirus; ebola virus; human herpesvirus (*e.g.*, HSV-1-9); human cytomegalovirus; human adenovirus; Epstein-Barr virus; hantaviruses; for animal, the animal counterpart to any above listed human virus, animal retroviruses, such as simian immunodeficiency virus, avian immunodeficiency virus, bovine immunodeficiency virus, feline immunodeficiency virus, equine infectious anemia virus, caprine arthritis encephalitis virus or visna virus.

The nucleic acids comprising cellular genes of this invention were isolated by the above method and as set forth in the examples. The invention includes a nucleic acid comprising the nucleotide sequence set forth in SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74 or SEQ ID NO:75 (this list is sometimes referred to herein as "SEQ ID NO:5 through SEQ ID NO:75" for brevity). Thus these nucleic acids can contain, in addition to the nucleotides set forth in each SEQ ID NO in the sequence listing, additional nucleotides at either end of the molecule. Such additional nucleotides can be added by any standard method, as known in the art, such as recombinant methods and synthesis methods. Examples of such nucleic acids

comprising the nucleotide sequence set forth in any entry of the sequence listing contemplated by this invention include, but are not limited to, for example, the nucleic acid placed into a vector; a nucleic acid having one or more regulatory region (*e.g.*, promoter, enhancer, polyadenylation site) linked to it, particularly in functional manner, *i.e.* such that an mRNA or a protein can be produced; a nucleic acid including additional nucleic acids of the gene, such as a larger or even full length genomic fragment of the gene, a partial or full length cDNA, a partial or full length RNA. Making and/or isolating such larger nucleic acids is further described below and is well known and standard in the art.

The invention also provides a nucleic acid encoding the protein encoded by the gene comprising the nucleotide sequence set forth in SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74 or SEQ ID NO:75 , as well as allelic variants and homologs of each such gene. The gene is readily obtained using standard methods, as described below and as is known and standard in the art. The present invention also contemplates any unique fragment of these genes or of the nucleic acids set forth in any of SEQ ID NO:5 through SEQ ID NO:75. Examples of inventive fragments of the inventive genes are the nucleic acids whose sequence is set forth in any of SEQ ID NO:5 through SEQ ID NO:75. To be unique, the fragment must be of

sufficient size to distinguish it from other known sequences, most readily determined by comparing any nucleic acid fragment to the nucleotide sequences of nucleic acids in computer databases, such as GenBank. Such comparative searches are standard in the art. Typically, a unique fragment useful as a primer or probe will be at least about 20 to about 25 nucleotides in length, depending upon the specific nucleotide content of the sequence. Additionally, fragments can be, for example, at least about 30, 40, 50, 75, 100, 200 or 500 nucleotides in length. The nucleic acids can be single or double stranded, depending upon the purpose for which it is intended.

The present invention further provides a nucleic acid comprising the regulatory region of a gene comprising the nucleotide sequences set forth in SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75. Additionally provided is a construct comprising such a regulatory region functionally linked to a reporter gene. Such reporter gene constructs can be used to screen for compounds and compositions that affect expression of the gene comprising the nucleic acids whose sequence is set forth in any of SEQ ID NO: 5 through SEQ ID NO: 75.

The nucleic acids set forth in the sequence listing are gene fragments; the entire coding sequence and the entire gene that comprises each fragment are both contemplated herein and are readily obtained by standard methods, given the nucleotide

sequences presented in the sequence listing (*see. e.g.*, Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1989; *DNA cloning: A Practical Approach*, Volumes I and II, Glover, D.M. ed., IRL Press Limited, Oxford, 1985). To obtain the entire genomic gene, briefly, a nucleic acid whose sequence is set forth in any of SEQ ID NO:1 through SEQ ID NO:83, or preferably in any of SEQ ID NO:5 through SEQ ID NO:83, or a smaller fragment thereof, is utilized as a probe to screen a genomic library under high stringency conditions, and isolated clones are sequenced. Once the sequence of the new clone is determined, a probe can be devised from a portion of the new clone not present in the previous fragment and hybridized to the library to isolate more clones containing fragments of the gene. In this manner, by repeating this process in organized fashion, one can "walk" along the chromosome and eventually obtain nucleotide sequence for the entire gene. Similarly, one can use portions of the present fragments, or additional fragments obtained from the genomic library, that contain open reading frames to screen a cDNA library to obtain a cDNA having the entire coding sequence of the gene. Repeated screens can be utilized as described above to obtain the complete sequence from several clones if necessary. The isolates can then be sequenced to determine the nucleotide sequence by standard means such as dideoxynucleotide sequencing methods (*see, e.g.*, Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1989).

The present genes were isolated from rat; however, homologs in any desired species, preferably mammalian, such as human, can readily be obtained by screening a human library, genomic or cDNA, with a probe comprising sequences of the nucleic acids set forth in the sequence listing herein, or fragments thereof, and isolating genes specifically hybridizing with the probe under preferably relatively high stringency hybridization conditions. For example, high salt conditions (*e.g.*, in 6X SSC or 6X SSPE) and/or high temperatures of hybridization can be used. For example, the stringency of hybridization is typically about 5°C to 20°C below the T_m (the melting temperature at which half of the molecules dissociate from its partner) for the given chain length. As is known in the art, the nucleotide composition of the hybridizing region factors in determining the melting temperature of the hybrid. For 20mer probes,

for example, the recommended hybridization temperature is typically about 55-58°C. Additionally, the rat sequence can be utilized to devise a probe for a homolog in any specific animal by determining the amino acid sequence for a portion of the rat protein, and selecting a probe with optimized codon usage to encode the amino acid sequence of the homolog in that particular animal. Any isolated gene can be confirmed as the targeted gene by sequencing the gene to determine it contains the nucleotide sequence listed herein as comprising the gene. Any homolog can be confirmed as a homolog by its functionality.

Additionally contemplated by the present invention are nucleic acids, from any desired species, preferably mammalian and more preferably human, having 98%, 95%, 90%, 85%, 80%, 70%, 60%, or 50% homology, or greater, in the region of homology, to a region in an exon of a nucleic acid encoding the protein encoded by the gene comprising the nucleotide sequence set forth in any of SEQ ID NO:5 through SEQ ID NO:75 of the sequence listing or to homologs thereof. Also contemplated by the present invention are nucleic acids, from any desired species, preferably mammalian and more preferably human, having 98%, 95%, 90%, 85%, 80%, 70%, 60%, or 50% homology, or greater, in the region of homology, to a region in an exon of a nucleic acid comprising the nucleotide sequence set forth in any of SEQ ID NO:5 through SEQ ID NO:75 of the sequence listing or to homologs thereof. These genes can be synthesized or obtained by the same methods used to isolate homologs, with stringency of hybridization and washing, if desired, reduced accordingly as homology desired is decreased, and further, depending upon the G-C or A-T richness of any area wherein variability is searched for. Allelic variants of any of the present genes or of their homologs can readily be isolated and sequenced by screening additional libraries following the protocol above. Methods of making synthetic genes are described in U.S. Patent No. 5,503,995 and the references cited therein.

The nucleic acid encoding any selected protein of the present invention can be any nucleic acid that functionally encodes that protein. For example, to functionally encode, *i.e.*, allow the nucleic acid to be expressed, the nucleic acid can include, for example, exogenous or endogenous expression control sequences, such as an origin of replication, a promoter, an enhancer, and necessary information processing sites, such as

ribosome binding sites, RNA splice sites, polyadenylation sites, and transcriptional terminator sequences. Preferred expression control sequences can be promoters derived from metallothionine genes, actin genes, immunoglobulin genes, CMV, SV40, adenovirus, bovine papilloma virus, etc. Expression control sequences can be selected for functionality in the cells in which the nucleic acid will be placed. A nucleic acid encoding a selected protein can readily be determined based upon the amino acid sequence of the selected protein, and, clearly, many nucleic acids will encode any selected protein.

The present invention additionally provides a nucleic acid that selectively hybridizes under stringent conditions with a nucleic acid encoding the protein encoded by the gene comprising the nucleotide sequence set forth in any sequence listed herein (*i.e.*, any of SEQ ID NO:5 through SEQ ID NO:75). This hybridization can be specific. The degree of complementarity between the hybridizing nucleic acid and the sequence to which it hybridizes should be at least enough to exclude hybridization with a nucleic acid encoding an unrelated protein. Thus, a nucleic acid that selectively hybridizes with a nucleic acid of the present protein coding sequence will not selectively hybridize under stringent conditions with a nucleic acid for a different, unrelated protein, and vice versa. Typically, the stringency of hybridization to achieve selective hybridization involves hybridization in high ionic strength solution (6X SSC or 6X SSPE) at a temperature that is about 12-25°C below the T_m (the melting temperature at which half of the molecules dissociate from its partner) followed by washing at a combination of temperature and salt concentration chosen so that the washing temperature is about 5°C to 20°C below the T_m of the hybrid molecule. The temperature and salt conditions are readily determined empirically in preliminary experiments in which samples of reference DNA immobilized on filters are hybridized to a labeled nucleic acid of interest and then washed under conditions of different stringencies. Hybridization temperatures are typically higher for DNA-RNA and RNA-RNA hybridizations. The washing temperatures can be used as described above to achieve selective stringency, as is known in the art. (Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1989; Kunkel et al. *Methods Enzymol.* 1987:154:367, 1987). Nucleic acid fragments that selectively

hybridize to any given nucleic acid can be used, *e.g.*, as primers and or probes for further hybridization or for amplification methods (*e.g.*, polymerase chain reaction (PCR), ligase chain reaction (LCR)) . A preferable stringent hybridization condition for a DNA:DNA hybridization can be at about 68°C (in aqueous solution) in 6X SSC or 6X SSPE followed by washing at 68°C.

The present invention additionally provides a protein encoded by a nucleic acid encoding the protein encoded by the gene comprising any of the nucleotide sequences set forth herein (*i.e.*., any of SEQ ID NO: 5 through SEQ ID NO:75). The protein can be readily obtained by any of several means. For example, the nucleotide sequence of coding regions of the gene can be translated and then the corresponding polypeptide can be synthesized mechanically by standard methods. Additionally, the coding regions of the genes can be expressed or synthesized, an antibody specific for the resulting polypeptide can be raised by standard methods (see, *e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1988), and the protein can be isolated from other cellular proteins by selective hybridization with the antibody. This protein can be purified to the extent desired by standard methods of protein purification (see, *e.g.*, Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1989). The amino acid sequence of any protein, polypeptide or peptide of this invention can be deduced from the nucleic acid sequence, or it can be determined by sequencing an isolated or recombinantly produced protein.

The terms “peptide,” "polypeptide"and "protein" are used interchangeably herein and refer to a polymer of amino acids and includes full-length proteins and fragments thereof. As used in the specification and in the claims, "a" can mean one or more, depending upon the context in which it is used. An amino acid residue is an amino acid formed upon chemical digestion (hydrolysis) of a polypeptide at its peptide linkages. The amino acid residues described herein are preferably in the "L" isomeric form. However, residues in the "D" isomeric form can be substituted for any L-amino acid residue, as long as the desired functional property is retained by the polypeptide. Standard polypeptide nomenclature (described in *J. Biol. Chem.*, 243:3552-59 (1969) and adopted at 37 CFR § 1.822(b)) is used herein.

As will be appreciated by those skilled in the art, the invention also includes those polypeptides having slight variations in amino acid sequences or other properties. Amino acid substitutions can be selected by known parameters to be neutral (*see, e.g.*, Robinson WE Jr, and Mitchell WM., AIDS 4:S151-S162(1990)). Such variations may arise naturally as allelic variations (*e.g.*, due to genetic polymorphism) or may be produced by human intervention (*e.g.*, by mutagenesis of cloned DNA sequences), such as induced point, deletion, insertion and substitution mutants. Minor changes in amino acid sequence are generally preferred, such as conservative amino acid replacements, small internal deletions or insertions, and additions or deletions at the ends of the molecules. Substitutions may be designed based on, for example, the model of Dayhoff, *et al.* (in *Atlas of Protein Sequence and Structure 1978*, Nat'l Biomed. Res. Found., Washington, D.C.). These modifications can result in changes in the amino acid sequence, provide silent mutations, modify a restriction site, or provide other specific mutations. Likewise, such amino acid changes result in a different nucleic acid encoding the polypeptides and proteins. Thus, alternative nucleic acids are also contemplated by such modifications.

The present invention also provides cells containing a nucleic acid of the invention. A cell containing a nucleic acid encoding a protein typically can replicate the DNA and, further, typically can express the encoded protein. The cell can be a prokaryotic cell, particularly for the purpose of producing quantities of the nucleic acid, or a eukaryotic cell, particularly a mammalian cell. The cell is preferably a mammalian cell for the purpose of expressing the encoded protein so that the resultant produced protein has mammalian protein processing modifications.

Nucleic acids of the present invention can be delivered into cells by any selected means, in particular depending upon the purpose of the delivery of the compound and the target cells. Many delivery means are well-known in the art. For example, electroporation, calcium phosphate precipitation, microinjection, cationic or anionic liposomes, and liposomes in combination with a nuclear localization signal peptide for delivery to the nucleus can be utilized, as is known in the art.

The present invention also contemplates that the mutated cellular genes necessary for viral growth, produced by the present method, as well as cells containing

these mutants can also be useful. These mutated genes and cells containing them can be isolated and/or produced according to the methods herein described and using standard methods.

It should be recognized that the sequences set forth herein may contain minor sequencing errors. Such errors can be corrected, for example, by using the hybridization procedure described above with various probes derived from the described sequences such that the coding sequence can be reisolated and resequenced.

As described in the examples, the present invention provides the discovery of a "serum survival factor" present in serum that is necessary for the survival of persistently virally infected cells. Isolation and characterization of this factor have shown it to be a protein, to have a molecular weight of between about 50 kD and 100 kD, to resist inactivation in low pH (*e.g.*, pH2) and chloroform extraction, to be inactivated by boiling for about 5 minutes and in low ionic strength solution (*e.g.*, about 10 mM to about 50 mM). The present invention thus provides a purified mammalian serum protein having a molecular weight of between about 50 kD and 100 kD which resists inactivation in low pH and resists inactivation by chloroform extraction, which inactivates when boiled and inactivates in low ionic strength solution, and which when removed from a cell culture comprising cells persistently infected with reovirus selectively substantially prevents survival of cells persistently infected with reovirus. The factor, fitting the physical characteristics described above, can readily be verified by adding it to non-serum-containing medium (which previously could not support survival of persistently virally infected cells) and determining whether this medium with the added putative factor can now support persistently virally infected cells, particularly cells persistently infected with reovirus. As used herein, a "purified" protein means the protein is at least of sufficient purity such that an approximate molecular weight can be determined.

The amino acid sequence of the protein can be elucidated by standard methods. For example, an antibody to the protein can be raised and used to screen an expression library to obtain nucleic acid sequence coding the protein. This nucleic acid sequence is then simply translated into the corresponding amino acid sequence. Alternatively, a portion of the protein can be directly sequenced by standard amino acid sequencing

methods (amino-terminus sequencing). This amino acid sequence can then be used to generate an array of nucleic acid probes that encompasses all possible coding sequences for a portion of the amino acid sequence. The array of probes is used to screen a cDNA library to obtain the remainder of the coding sequence and thus ultimately the corresponding amino acid sequence.

The present invention also provides methods of detecting and isolating additional serum survival factors. For example, to determine if any known serum components are necessary for viral growth, the known components can be inhibited in, or eliminated from, the culture medium, and it can be observed whether viral growth is inhibited by determining if persistently infected cells do not survive. One can add the factor back (or remove the inhibition) and determine whether the factor allows for viral growth.

Additionally, other, unknown serum components can also be found to be essential for viral growth. Serum can be fractionated by various standard means, and fractions added to serum free medium to determine if a factor is present in a reaction that allows viral growth previously inhibited by the lack of serum. Fractions having this activity can then be further fractionated until the factor is relatively free of other components. The factor can then be characterized by standard methods, such as size fractionation, denaturation and/or inactivation by various means, etc. Preferably, once the factor has been purified to a desired level of purity, it is added to cells in serum free medium to confirm that it bestows the function of allowing virus to grow when serum-free medium alone did not. This method can be repeated to confirm the requirement for the specific factor for any desired virus, since each serum factor found to be required by any one virus can also be required by many other viruses. In general, the closer the viruses are related and the more similar the infection modes of the viruses, the more likely that a factor required by one virus will be required by the other.

The present invention also provides methods of treating virus infections utilizing applicants' discoveries. The subject of any of the herein described methods can be any animal, preferably a mammal, such as a human, a veterinary animal, such as a cat, dog, horse, pig, goat, sheep, or cow, or a laboratory animal, such as a mouse, rat, rabbit, or guinea pig, depending upon the virus.

The present invention provides a method of reducing or inhibiting, and thereby treating, a viral infection in a subject, comprising administering to the subject an inhibiting amount of a composition that inhibits functioning of the serum protein described herein, *i.e.* the serum protein having a molecular weight of between about 50 kD and 100 kD which resists inactivation in low pH and resists inactivation by chloroform extraction, which inactivates when boiled and inactivates in low ionic strength solution, and which when removed from a cell culture comprising cells persistently infected with the virus prevents survival of at least some cells persistently infected with the virus, thereby treating the viral infection. The composition can comprise, for example, an antibody that specifically binds the serum protein, or an antisense RNA that binds an RNA encoded by a gene functionally encoding the serum protein

Any virus capable of infecting the selected subject to be treated can be treated by the present method. As described above, any serum protein or survival factor found by the present methods to be necessary for growth of any one virus can be found to be necessary for growth of many other viruses. For any given virus, the serum protein or factor can be confirmed to be required for growth by the methods described herein. The cellular genes identified by the examples using reovirus, a mammalian pathogen, and a rat cell system have general applicability to other virus infections that include all of the known as well as yet to be discovered human pathogens, including, but not limited to: human immunodeficiency viruses (*e.g.*, HIV-1, HIV-2); parvovirus; papillomaviruses; hantaviruses; influenza viruses (*e.g.*, influenza A, B and C viruses); hepatitis viruses A to G; caliciviruses; astroviruses; rotaviruses; coronaviruses, such as human respiratory coronavirus; picornaviruses, such as human rhinovirus and enterovirus; ebola virus; human herpesvirus (*e.g.*, HSV-1-9); human cytomegalovirus; human adenovirus; Epstein-Barr virus; hantaviruses; for animal, the animal counterpart to any above listed human virus, animal retroviruses, such as simian immunodeficiency virus, avian immunodeficiency virus, bovine immunodeficiency virus, feline immunodeficiency virus, equine infectious anemia virus, caprine arthritis encephalitis virus or visna virus.

A protein inhibiting amount of the composition can be readily determined, such as by administering varying amounts to cells or to a subject and then adjusting the

effective amount for inhibiting the protein according to the volume of blood or weight of the subject. Compositions that bind to the protein can be readily determined by running the putatively bound protein on a protein gel and observing an alteration in the protein's migration through the gel. Inhibition of the protein can be determined by any desired means such as adding the inhibitor to complete media used to maintain persistently infected cells and observing the cells' viability. The composition can comprise, for example, an antibody that specifically binds the serum protein. Specific binding by an antibody means that the antibody can be used to selectively remove the factor from serum or inhibit the factor's biological activity and can readily be determined by radio immune assay (RIA), bioassay, or enzyme-linked immunosorbant (ELISA) technology. The composition can comprise, for example, an antisense RNA that specifically binds an RNA encoded by the gene encoding the serum protein. Antisense RNAs can be synthesized and used by standard methods (*e.g.*, *Antisense RNA and DNA*, D. A. Melton, Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1988)).

The present methods provide a method of screening a compound for treating a viral infection, comprising administering the compound to a cell containing a cellular gene functionally encoding a gene product necessary for reproduction of the virus in the cell but not necessary for survival of the cell and detecting level of the gene product produced, a decrease or elimination of the gene product indicating a compound for treating the viral infection. The present methods also provide a method of screening a compound for effectiveness in treating a viral infection, comprising administering the compound to a cell containing a cellular gene functionally encoding a gene product necessary for reproduction of the virus in the cell but not necessary for survival of the cell and detecting the level of the gene product produced, a decrease or elimination of the gene product indicating a compound effective for treating the viral infection. The cellular gene can be, for example, any gene provided herein, *i.e.*, any of the genes comprising the nucleotide sequences set forth in any of SEQ ID NO:1 through SEQ ID NO:75, or any other gene obtained using the methods provided herein for obtaining such genes. Level of the gene product can be measured by any standard means, such as by detection with an antibody specific for the protein. The level of gene product can be compared to the level of the gene product in a control cell not contacted with the

compound. The level of gene product can be compared to the level of the gene product in the same cell prior to addition of the compound. Relatedly, the regulatory region of the gene can be functionally linked to a reporter gene and compounds can be screened for inhibition of the reporter gene. Such reporter constructs are described herein.

The present invention provides a method of selectively eliminating cells persistently infected with a virus from an animal cell culture capable of surviving for a first period of time in the absence of serum, comprising propagating the cell culture in the absence of serum for a second time period which a persistently infected cell cannot survive without serum, thereby selectively eliminating from the cell culture cells persistently infected with the virus. The second time period should be shorter than the first time period. Thus one can simply eliminate serum from a standard culture medium composition for a period of time (*e.g.* by removing serum containing medium from the culture container, rinsing the cells, and adding serum-free medium back to the container), then, after a time of serum starvation, return serum to the culture medium. Alternatively, one can inhibit a serum survival factor from the culture in place of the step of serum starvation. Furthermore, one can instead interfere with the virus-factor interaction. Such a viral elimination method can periodically be performed for cultured cells to ensure that they remain virus-free. The time period of serum removal can greatly vary, with a typical range being about 1 to about 30 days; a preferable period can be about 3 to about 10 days, and a more preferable period can be about 5 days to about 7 days. This time period can be selected based upon ability of the specific cell to survive without serum as well as the life cycle of the virus, *e.g.*, for reovirus, which has a life cycle of about 24 hours, 3 days' starvation of cells provides dramatic results.

Furthermore, the time period can be shortened by also passaging the cells during the starvation; in general, increasing the number of passages can decrease the time of serum starvation (or serum factor inhibition) needed to get full clearance of the virus from the culture. While passaging, the cells typically are exposed briefly to serum (typically for about 3 to about 24 hours). This exposure both stops the action of the trypsin used to dislodge the cells and stimulates the cells into another cycle of growth, thus aiding in this selection process. Thus a starvation/serum cycle can be repeated to optimize the selective effect. Other standard culture parameters, such as confluency of

the cultures, pH, temperature, etc. can be varied to alter the needed time period of serum starvation (or serum survival factor inhibition). This time period can readily be determined for any given viral infection by simply removing the serum for various periods of time, then testing the cultures for the presence of the infected cells (*e.g.*, by ability to survive in the absence of serum and confirmed by quantitating virus in cells by standard virus titration and immunohistochemical techniques) at each tested time period, and then detecting at which time periods of serum deprivation the virally infected cells were eliminated. It is preferable that shorter time periods of serum deprivation that still provide elimination of the persistently infected cells be used. Furthermore, the cycle of starvation, then adding back serum and determining amount of virus remaining in the culture can be repeated until no virtually infected cells remain in the culture.

Thus, the present method can further comprise passaging the cells, *i.e.*, transferring the cell culture from a first container to a second container. Such transfer can facilitate the selective lack of survival of virally infected cells. Transfer can be repeated several times. Transfer is achieved by standard methods of tissue culture (*see, e.g.*, Freshney, *Culture of Animal Cells, A Manual of Basic Technique*, 2nd Ed. Alan R. Liss, Inc., New York, 1987).

The present method further provides a method of selectively eliminating from a cell culture cells persistently infected with a virus, comprising propagating the cell culture in the absence of a functional form of the serum protein having a molecular weight of between about 50 kD and 100 kD which resists inactivation in low pH and resists inactivation by chloroform extraction, which inactivates when boiled and inactivates in low ionic strength solution, and which when removed from a cell culture comprising cells persistently infected with reovirus substantially prevents survival of cells persistently infected with reovirus. The absence of the functional form can be achieved by any of several standard means, such as by binding the protein to an antibody selective for it (binding the antibody in serum either before or after the serum is added to the cells; if before, the serum protein can be removed from the serum by, *e.g.*, binding the antibody to a column and passing the serum over the column and then administering the survival protein-free serum to the cells), by administering a compound that

inactivates the protein, or by administering a compound that interferes with the interaction between the virus and the protein.

Thus, the present invention provides a method of selectively eliminating from a cell culture propagated in serum-containing medium cells persistently infected with a virus, comprising inhibiting in the serum the protein having a molecular weight of between about 50 kD and 100 kD which resists inactivation in low pH and resists inactivation by chloroform extraction, which inactivates when boiled and inactivates in low ionic strength solution, and which when removed from a cell culture comprising cells persistently infected with reovirus substantially prevents survival of cells persistently infected with reovirus. Alternatively, the interaction between the virus and the serum protein can be disrupted to selectively eliminate cells persistently infected with the virus.

Any virus capable of some form of persistent infection may be eliminated from a cell culture utilizing the present elimination methods, including removing, inhibiting or otherwise interfering with a serum protein, such as the one exemplified herein, and also including removing, inhibiting or otherwise interfering with a gene product from any cellular gene found by the present method to be necessary for viral growth yet nonessential to the cell. For example, DNA viruses or RNA viruses can be targeted. One can readily determine whether cells infected with a selected virus can be selectively removed from a culture through removal of serum by starving cells permissive to the virus of serum (or inhibiting the serum survival factor), adding the selected virus to the cells, adding serum to the culture, and observing whether infected cells die (*i.e.*, by titering levels of virus in the surviving cells with an antibody specific for the virus).

A culture of any animal cell (*i.e.*, any cell that is typically grown and maintained in culture in serum) that can be maintained for a period of time in the absence of serum, can be purified from viral infection utilizing the present method. For example, primary cultures as well as established cultures and cell lines can be used. Furthermore, cultures of cells from any animal and any tissue or cell type within that animal that can be cultured and that can be maintained for a period of time in the absence of serum can be used. For example, cultures of cells from tissues typically infected, and particularly persistently infected, by an infectious virus could be used.

As used in the claims "in the absence of serum" means at a level at which persistently virally infected cells do not survive. Typically, the threshold level is about 1% serum in the media. Therefore, about 1% serum or less can be used, such as about 1%, 0.75%, 0.50%. 0.25% 0.1% or no serum can be used.

As used herein, "selectively eliminating" cells persistently infected with a virus means that substantially all of the cells persistently infected with the virus are killed such that the presence of virally infected cells cannot be detected in the culture immediately after the elimination procedure has been performed. Furthermore, "selectively eliminating" includes that cells not infected with the virus are generally not killed by the method. Some surviving cells may still produce virus but at a lower level, and some may be defective in pathways that lead to death by the virus. Typically, for cells persistently infected with virus to be substantially all killed, more than about 90% of the cells, and more preferably less than about 95%, 98%, 99%, or 99.99% of virus-containing cells in the culture are killed.

The present method also provides a nucleic acid comprising the regulatory region of any of the genes. Such regulatory regions can be isolated from the genomic sequences isolated and sequenced as described above and identified by any characteristics observed that are characteristic for regulatory regions of the species and by their relation to the start codon for the coding region of the gene. The present invention also provides a construct comprising the regulatory region functionally linked to a reporter gene. Such constructs are made by routine subcloning methods, and many vectors are available into which regulatory regions can be subcloned upstream of a marker gene. Marker genes can be chosen for ease of detection of marker gene product.

The present method therefore also provides a method of screening a compound for treating a viral infection, comprising administering the compound to a cell containing any of the above-described constructs, comprising a regulatory region of one of the genes comprising the nucleotide sequence set forth in any of SEQ ID NO:1 through SEQ ID NO:75 functionally linked to a reporter gene, and detecting the level of the reporter gene product produced, a decrease or elimination of the reporter gene product indicating a compound for treating the viral infection. Compounds detected by this method would inhibit transcription of the gene from which the regulatory region was

isolated, and thus, in treating a subject, would inhibit the production of the gene product produced by the gene, and thus treat the viral infection.

The present invention additionally provides a method of reducing or inhibiting a viral infection in a subject, comprising administering to the subject an amount of a composition that inhibits expression or functioning of a gene product encoded by a gene comprising the nucleic acid set forth in any of SEQ ID NO:1 through SEQ ID NO:75, or a homolog thereof, thereby treating the viral infection. the composition can comprise, for example, an antibody that binds a protein encoded by the gene. The composition can also comprise an antibody that binds a receptor for a protein encoded by the gene. Such an antibody can be raised against the selected protein by standard methods, and can be either polyclonal or monoclonal, though monoclonal is preferred. Alternatively, the composition can comprise an antisense RNA that binds an RNA encoded by the gene. Furthermore, the composition can comprise a nucleic acid functionally encoding an antisense RNA that binds an RNA encoded by the gene. Other useful compositions will be readily apparent to the skilled artisan.

The present invention further provides a method of reducing or inhibiting a viral infection in a subject comprising mutating *ex vivo* in a selected cell from the subject an endogenous gene comprising the nucleic acid set forth in any of SEQ ID NO:1 through SEQ ID NO:75, or a homolog thereof, to a gene form incapable of producing a functional gene product of the gene or a gene form producing a reduced amount of a functional gene product of the gene, and replacing the cell in the subject, thereby reducing viral infection of cells in the subject. The cell can be selected according to the typical target cell of the specific virus whose infection is to be reduced, prevented or inhibited. A preferred cell for several viruses is a hematopoietic cell. When the selected cell is a hematopoietic cell, viruses which can be reduced or inhibited from infection can include, for example, HIV, including HIV-1 and HIV-2.

The present invention also provides a method of reducing or inhibiting a viral infection in a subject comprising mutating *ex vivo* in a selected cell from the subject an endogenous gene comprising a nucleic acid isolated by a method comprising (a) transferring into a cell culture growing in serum-containing medium a vector encoding a selective marker gene lacking a functional promoter, (b) selecting cells

expressing the marker gene, (c) removing serum from the culture medium, (d) infecting the cell culture with the virus, and (e) isolating from the surviving cells a cellular gene within which the marker gene is inserted,

to a mutated gene form incapable of producing a functional gene product of the gene or to a mutated gene form producing a reduced amount of a functional gene product of the gene, and replacing the cell in the subject, thereby reducing viral infection of cells in the subject. Thus the mutated gene form can be one incapable of producing an effective amount of a functional protein or mRNA, or one incapable of producing a functional protein or mRNA, for example. The method can be performed wherein the virus is HIV. The method can be performed in any selected cell in which the virus may infect with deleterious results. For example, the cell can be a hematopoietic cell. However, many other virus-cell combinations will be apparent to the skilled artisan. **[Dr. Rubin: any other virus-cell relationships particularly good targets for this method?]**

The present invention additionally provides a method of increasing viral infection resistance in a subject comprising mutating *ex vivo* in a selected cell from the subject an endogenous gene comprising a nucleic acid isolated by a method comprising (a) transferring into a cell culture growing in serum-containing medium a vector encoding a selective marker gene lacking a functional promoter, (b) selecting cells expressing the marker gene, (c) removing serum from the culture medium, (d) infecting the cell culture with the virus, and (e) isolating from the surviving cells a cellular gene within which the marker gene is inserted,

to a mutated gene form incapable of producing a functional gene product of the gene or a gene form producing a reduced amount of a functional gene product of the gene, and replacing the cell in the subject, thereby reducing viral infection of cells in the subject. The virus can be HIV, particularly when the cell is a hematopoietic cell. However, many other virus-cell combinations will be apparent to the skilled artisan.

The present invention provides a method of identifying a cellular gene that can suppress a malignant phenotype in a cell, comprising (a) transferring into a cell culture incapable of growing well in soft agar or Matrigel a vector encoding a selective marker gene lacking a functional promoter, (b) selecting cells expressing the marker gene, and (c) isolating from selected cells which are capable of growing in soft agar or Matrigel a

cellular gene within which the marker gene is inserted, thereby identifying a gene that can suppress a malignant phenotype in a cell. This method can be performed using any selected non-transformed cell line, of which many are known in the art.

The present invention additionally provides a method of identifying a cellular gene that can suppress a malignant phenotype in a cell, comprising (a) transferring into a cell culture of non-transformed cells a vector encoding a selective marker gene lacking a functional promoter, (b) selecting cells expressing the marker gene, and (c) isolating from selected and transformed cells a cellular gene within which the marker gene is inserted, thereby identifying a gene that can suppress a malignant phenotype in a cell. A non-transformed phenotype can be determined by any of several standard methods in the art, such as the exemplified inability to grow in soft agar, or inability to grow in Matrigel.

The present invention further provides a method of screening for a compound for suppressing a malignant phenotype in a cell comprising administering the compound to a cell containing a cellular gene functionally encoding a gene product involved in establishment of a malignant phenotype in the cell and detecting the level of the gene product produced, a decrease or elimination of the gene product indicating a compound effective for suppressing the malignant phenotype. Detection of the level, or amount, of gene product produced can be measured, directly or indirectly, by any of several methods standard in the art (*e.g.*, protein gel, antibody-based assay, detecting labeled RNA) for assaying protein levels or amounts, and selected based upon the specific gene product.

The present invention further provides a method of suppressing a malignant phenotype in a cell in a subject, comprising administering to the subject an amount of a composition that inhibits expression or functioning of a gene product encoded by a gene comprising the nucleic acid set forth in SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82 or SEQ ID NO:83, or a homolog thereof, thereby suppressing a malignant phenotype. The composition can, for example, comprise an antibody that binds a protein encoded by the gene. The composition can, as another example, comprise an antibody that binds a receptor for a protein encoded by the gene. The composition can comprise an antisense

RNA that binds an RNA encoded by the gene. Further, the composition can comprise a nucleic acid functionally encoding an antisense RNA that binds an RNA encoded by the gene.

Diagnostic or therapeutic agents of the present invention can be administered to a subject or an animal model by any of many standard means for administering therapeutics or diagnostics to that selected site or standard for administering that type of functional entity. For example, an agent can be administered orally, parenterally (e.g., intravenously), by intramuscular injection, by intraperitoneal injection, topically, transdermally, or the like. Agents can be administered, *e.g.*, as a complex with cationic liposomes, or encapsulated in anionic liposomes. Compositions can include various amounts of the selected agent in combination with a pharmaceutically acceptable carrier and, in addition, if desired, may include other medicinal agents, pharmaceutical agents, carriers, adjuvants, diluents, etc. Parental administration, if used, is generally characterized by injection. Injectables can be prepared in conventional forms, either as liquid solutions or suspensions, solid forms suitable for solution or suspension in liquid prior to injection, or as emulsions. Depending upon the mode of administration, the agent can be optimized to avoid degradation in the subject, such as by encapsulation, etc.

Dosages will depend upon the mode of administration, the disease or condition to be treated, and the individual subject's condition, but will be that dosage typical for and used in administration of antiviral or anticancer agents. Dosages will also depend upon the composition being administered, *e.g.*, a protein or a nucleic acid. Such dosages are known in the art. Furthermore, the dosage can be adjusted according to the typical dosage for the specific disease or condition to be treated. Furthermore, viral titers in culture cells of the target cell type can be used to optimize the dosage for the target cells *in vivo*, and transformation from varying dosages achieved in culture cells of the same type as the target cell type can be monitored. Often a single dose can be sufficient; however, the dose can be repeated if desirable. The dosage should not be so large as to cause adverse side effects. Generally, the dosage will vary with the age, condition, sex and extent of the disease in the patient and can be determined by

one of skill in the art. The dosage can also be adjusted by the individual physician in the event of any complication.

For administration to a cell in a subject, the composition, once in the subject, will of course adjust to the subject's body temperature. For *ex vivo* administration, the composition can be administered by any standard methods that would maintain viability of the cells, such as by adding it to culture medium (appropriate for the target cells) and adding this medium directly to the cells. As is known in the art, any medium used in this method can be aqueous and non-toxic so as not to render the cells non-viable. In addition, it can contain standard nutrients for maintaining viability of cells, if desired. For *in vivo* administration, the complex can be added to, for example, a blood sample or a tissue sample from the patient, or to a pharmaceutically acceptable carrier, e.g., saline and buffered saline, and administered by any of several means known in the art. Examples of administration include parenteral administration, e.g., by intravenous injection including regional perfusion through a blood vessel supplying the tissues(s) or organ(s) having the target cell(s), or by inhalation of an aerosol, subcutaneous or intramuscular injection, topical administration such as to skin wounds and lesions, direct transfection into, e.g., bone marrow cells prepared for transplantation and subsequent transplantation into the subject, and direct transfection into an organ that is subsequently transplanted into the subject. Further administration methods include oral administration, particularly when the composition is encapsulated, or rectal administration, particularly when the composition is in suppository form. A pharmaceutically acceptable carrier includes any material that is not biologically or otherwise undesirable, i.e., the material may be administered to an individual along with the selected complex without causing any undesirable biological effects or interacting in a deleterious manner with any of the other components of the pharmaceutical composition in which it is contained.

Specifically, if a particular cell type *in vivo* is to be targeted, for example, by regional perfusion of an organ or tumor, cells from the target tissue can be biopsied and optimal dosages for import of the complex into that tissue can be determined *in vitro*, as described herein and as known in the art, to optimize the *in vivo* dosage, including

concentration and time length. Alternatively, culture cells of the same cell type can also be used to optimize the dosage for the target cells *in vivo*.

For either *ex vivo* or *in vivo* use, the complex can be administered at any effective concentration. An effective concentration is that amount that results in reduction, inhibition or prevention of the viral infection or in reduction or inhibition of transformed phenotype of the cells

A nucleic acid can be administered in any of several means, which can be selected according to the vector utilized, the organ or tissue, if any, to be targeted, and the characteristics of the subject. The nucleic acids, if desired in a pharmaceutically acceptable carrier such as physiological saline, can be administered systemically, such as intravenously, intraarterially, orally, parenterally, subcutaneously. The nucleic acids can also be administered by direct injection into an organ or by injection into the blood vessel supplying a target tissue. For an infection of cells of the lungs or trachea, it can be administered intratracheally. The nucleic acids can additionally be administered topically, transdermally, etc.

The nucleic acid or protein can be administered in a composition. For example, the composition can comprise other medicinal agents, pharmaceutical agents, carriers, adjuvants, diluents, etc. Furthermore, the composition can comprise, in addition to the vector, lipids such as liposomes, such as cationic liposomes (e.g., DOTMA, DOPE, DC-cholesterol) or anionic liposomes. Liposomes can further comprise proteins to facilitate targeting a particular cell, if desired. Administration of a composition comprising a vector and a cationic liposome can be administered to the blood afferent to a target organ or inhaled into the respiratory tract to target cells of the respiratory tract. Regarding liposomes, see, e.g., Brigham et al. *Am. J. Resp. Cell. Mol. Biol.* 1:95-100 (1989); Felgner et al. *Proc. Natl. Acad. Sci USA* 84:7413-7417 (1987); U.S. Pat. No.4,897,355.

For a viral vector comprising a nucleic acid, the composition can comprise a pharmaceutically acceptable carrier such as phosphate buffered saline or saline. The viral vector can be selected according to the target cell, as known in the art. For example, adenoviral vectors, in particular replication-deficient adenoviral vectors, can be

utilized to target any of a number of cells, because of its broad host range. Many other viral vectors are available, and their target cells known..

EXAMPLES

Selective elimination of virally infected cells from a cell culture

Rat intestinal cell line-1 cells (RIE-1 cells) were standardly grown in Dulbecco's modified eagle's medium, high glucose, supplemented with 10% fetal bovine serum. To begin the experiment, cells persistently infected with reovirus were grown to near confluence, then serum was removed from the growth medium by removing the medium, washing the cells in PBS, and returning to the flask medium not supplemented with serum. Typically, the serum content was reduced to 1% or less. The cells are starved for serum for several days, or as long as about a month, to bring them to quiescence or growth arrest. Media containing 10% serum is then added to the quiescent cells to stimulate growth of the cells. Surviving cells are found to not to be persistently infected cells by immunohistochemical techniques used to establish whether cells contain any infectious virus (sensitivity to 1 infectious virus per ml of homogenized cells).

Cellular Genomic DNA Isolation

Gene Trap Libraries: The libraries are generated by infecting the RIE-1 cells with a retrovirus vector (U3 gene-trap) at a ratio of less than one retrovirus for every ten cells. When a U3 gene trap retrovirus integrates within an actively transcribed gene, the neomycin resistance gene that the U3 gene trap retrovirus encodes is also transcribed, this confers resistance to the cell to the antibiotic neomycin. Cells with gene trap events are able to survive exposure to neomycin while cells without a gene trap event die. The various cells that survive neomycin selection are then propagated as a library of gene trap events. Such libraries can be generated with any retrovirus vector that has the properties of expressing a reporter gene from a transcriptionally active cellular promoter that tags the gene for later identification.

Reovirus selection: Reovirus infection is typically lethal to RIE-1 cells but can result in the development of persistently infected cells. These cells continue to grow while producing infective reovirus particles. For the identification of gene trap events

that confer reovirus resistance to cells, the persistently infected cells must be eliminated or they will be scored as false positives. We have found that RIE-1 cells persistently infected with reovirus are very poorly tolerant to serum starvation, passaging and plating at low density. Thus, we have developed protocols for the screening of the RIE-1 gene trap libraries that select against both reovirus sensitive cells and cells that are persistently infected with reovirus.

1. RIE-1 library cells are grown to near confluence and then the serum is removed from the media. The cells are starved for serum for several days to bring them to quiescent or growth arrest.
2. The library cells are infected with reovirus at a titer of greater than ten reovirus per cell and the serum starvation is continued for several more days.
3. The infected cells are passaged, (a process in which they are exposed to serum for three to six hours) and then starved for serum for several more days.
4. The surviving cells are then allowed to grow in the presence of serum until visible colonies develop at which point they are cloned by limiting dilution.

MEDIA: DULBECCO'S MODIFIED EAGLE'S MEDIUM, HIGH GLUCOSE (DME/HIGH) Hyclone Laboratories cat. no. SH30003.02.

NEOMYCIN: The antibiotic used to select against the cells that did not have a U3 gene trap retrovirus. We used GENETICIN, from Sigma. cat. no. G9516.

RAT INTESTINAL CELL LINE-1 CELLS (RIE-1 CELLS): These cells are from the laboratory of Dr. Ray Dubois (VAMC). They are typically cultured in Dulbecco's Modified Eagle's Medium supplemented with 10% fetal calf serum.

REOVIRUS: Laboratory strains of either serotype 1 or serotype 3 are used. They were originally obtained from the laboratories of Bernard N. Fields (deceased). These viruses have been described in detail.

RETROVIRUS: The U3 gene trap retrovirus used here were developed by Dr. Earl Ruley (VAMC) and the libraries were produced using a general protocol suggested by him.

SERUM: FETAL BOVINE SERUM Hyclone Laboratories cat. no. A-1115-L.

Genes Necessary for Viral Infection

Characteristics of some of the isolated sequences include the following:

SEQ ID NO:1- rat genomic sequence of vacuolar H+ATPase (chemically inhibiting the activity of the gene product results in resistance to influenza virus and reovirus)

SEQ ID NO:2- rat alpha tropomyosin genomic sequence

SEQ ID NO:3- rat genomic sequence of murine and rat gas5 gene (cell cycle regulated gene)

SEQ ID NO:4- rat genomic sequence of p162 of ras complex , mouse, human (cell cycle regulated gene)

SEQ ID NO:5- similar to N-acetyl-glucosaminyltransferase I mRNA, mouse, human (enzyme located in the Golgi region in the cell; has been found as part of a DNA containing virus)

SEQ ID NO:6- similar to calcyclin, mouse, human, reverse complement (cell cycle regulated gene)

SEQ ID NO:7- contains sequence similar to :LOCUS AA254809 364 bp mRNA EST DEFINITION mz75a10.r1 Soares mouse lymph node NbMLN Mus musculus cDNA clone 719226 5'

SEQ ID NO:8- contains a sequence similar to No SW:RSP1_MOUSE Q01730 RSP-1 PROTEIN

SEQ ID NO:9- contains 5' UTR of gb|U25435|HSU25435 Human transcriptional repressor (CTCF) mRNA, complete cds, Length = 3780

SEQ ID NO:38- similar to cDNA of retroviral origin

SEQ ID NO: 50- trapped AYU-6 genetic element

Isolation of cellular genes that suppress a malignant phenotype

We have utilized a gene-trap method of selecting cell lines that have a transformed phenotype (are potentially tumor cells) from a population of cells (RIE-1 parentals) that are not transformed. The parental cell line, RIE-1 cells, does not have the capacity to grow in soft agar or to produce tumors in mice. Following gene-trapping, cells were screened for their capacity to grow in soft agar. These cells were cloned and genomic sequences were obtained 5' or 3' of the retrovirus vector (SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID

NO:81, SEQ ID NO:82, SEQ ID NO:83). All of the cell lines behave as if they are tumor cell lines, as they also induce tumors in mice.

Of the cell lines, two are associated with the enhanced expression of the prostaglandin synthetase gene II or COX 2. The COX 2 gene has been found to be increased in pre-malignant adenomas in humans and overexpressed in human colon cancer. Inhibitors of COX 2 expression also arrests the growth of the tumor. One of the cell lines, x18 (SEQ ID NO:76), has disrupted a gene that is now represented in the EST (dbest) database, but the gene is not known (not present in GenBank). (SEQ ID NO:76): >02-X18H-t7.., identical to: gb|W55397|W55397 mb13h04.r1 Life Tech mouse brain Mus at 1.0e-114. x18 has also been sequenced from the vector with the same EST being found. (SEQ ID NO:77): >x8_b4_2.. (SEQ ID NO:78): >x7_b4.. (SEQ ID NO:79): >x4-b4.. (SEQ ID NO:80): >x2-b4... (SEQ ID NO:81): >x15-b4.. (SEQ ID NO:82): >x13-re.., reverse complement. (SEQ ID NO:83): >x12_b4..

Each of the genes from which the provided nucleotide sequences is isolated represents a tumor suppressor gene. The mechanism by which the disrupted genes other than the gene comprising the nucleic acid which sequence is set forth in SEQ ID NO:76 may suppress a transformed phenotype is at present unknown. However, each one represents a tumor suppressor gene that is potentially unique, as none of the genomic sequences correspond to a known gene. The capacity to select quickly tumor suppressor genes may provide unique targets in the process of treating or preventing (potential for diagnostic testing) cancer.

Isolation of entire genomic genes

An isolated nucleic acid of this invention (whose sequence is set forth in any of SEQ ID NO:1 through SEQ ID NO: 83), or a smaller fragment thereof, is labeled by a detectable label and utilized as a probe to screen a rat genomic library (lambda phage or yeast artificial chromosome vector library) under high stringency conditions, *i.e.*, high salt and high temperatures to create hybridization and wash temperature 5-20°C. Clones are isolated and sequenced by standard Sanger dideoxynucleotide sequencing

methods. Once the entire sequence of the new clone is determined, it is aligned with the probe sequence and its orientation relative to the probe sequence determined. A second and third probe is designed using sequences from either end of the combined genomic sequence, respectively. These probes are used to screen the library, isolate new clones, which are sequenced. These sequences are aligned with the previously obtained sequences and new probes designed corresponding to sequences at either end and the entire process repeated until the entire gene is isolated and mapped. When one end of the sequence cannot isolate any new clone, a new library can be screened. The complete sequence includes regulatory regions at the 5' end and a polyadenylation signal at the 3' end.

Isolation of cDNAs

An isolated nucleic acid (whose sequence is set forth in any of SEQ ID NO:1 through SEQ ID NO:83, and preferably any of SEQ ID NO:5 through SEQ ID NO:83), or a smaller fragment thereof, or additional fragments obtained from the genomic library, that contain open reading frames, is labeled by a detectable label and utilized as a probe to screen a portions of the present fragments, to screen a cDNA library. A rat cDNA library obtains rat cDNA; a human cDNA library obtains a human cDNA. Repeated screens can be utilized as described above to obtain the complete coding sequence of the gene from several clones if necessary. The isolates can then be sequenced to determine the nucleotide sequence by standard means such as dideoxynucleotide sequencing methods.

Serum survival factor isolation and characterization

The lack of tolerance to serum starvation is due to the acquired dependence of the persistently infected cells for a serum factor (survival factor) that is present in serum. The serum survival factor for persistently infected cells has a molecular weight between 50 and 100 kD and resists inactivation in low pH (pH2) and chloroform extraction. It is inactivated by boiling for 5 minutes [once fractionated from whole serum (50 to 100 kD fraction)], and in low ionic strength solution [10 to 50 mM].

The factor was isolated from serum by size fraction using centriprep molecular cut-off filters with excluding sizes of 30 and 100 kd (Millipore and Amnicon), and dialysis tubing with a molecular exclusion of 50 kd. Polyacrylamide gel electrophoresis and silver staining was used to determine that all of the resulting material was between 50 and 100 kd, confirming the validity of the initial isolation. Further purification was performed on using ion exchange chromatography, and heparin sulfate adsorption columns, followed by HPLC. Activity was determined following adjusting the pH of the serum fraction (30 to 100 kd fraction) to different pH conditions using HCl and readjusting the pH to pH 7.4 prior to assessment of biologic activity. Low ionic strength sensitivity was determined by dialyzing the fraction containing activity into low ionic strength solution for various lengths of time and readjusting ionic strength to physiologic conditions prior to determining biologic activity by dialyzing the fraction against the media. The biologic activity was maintained in the aqueous solution following chloroform extraction, indicating the factor is not a lipid. The biologic activity was lost after the 30 to 100 kd fraction was placed in a 100°C water bath for 5 minutes.

Isolated nucleic acids

Tagged genomic DIAS isolated were sequenced by standard methods using Sanger dideoxynucleotide sequencing. The nucleotide sequences of these nucleic acids are set forth herein as SEQ ID NO:1 through SEQ ID NO:75 (viral infection genes) and SEQ ID NO:76 through SEQ ID NO:83 (tumor suppressor genes). The sequences were run through computer databanks in a homology search. Sequences for some of the "6b" sequences [obtained from genomic library 6, flask b] (*i.e.*, SEQ ID NO:37, 38, 39, 42, 61, 65, 66, 69) correspond to a known gene, alpha tropomyosin, and some of the others correspond to the vacuolar-H^+-ATPase. These sequences are associated with both acute and persistent viral infection and the cellular genes which comprise them. *i.e.*, alpha tropomyosin and vacuolar-H^+-ATPase, can be targets for drug treatments for viral infection using the methods described above. These genes can be therapy targets particularly because disruption of one or both alleles results in a viable cell.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: VANDERBILT UNIVERSITY
305 Kirkland Hall
Nashville, TN 37240

(ii) TITLE OF INVENTION: MAMMALIAN GENES INVOLVED IN VIRAL INFECTION

(iii) NUMBER OF SEQUENCES: 83

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Needle & Rosenberg, P.C.
(B) STREET: 127 Peachtree Street, Suite 1200
(C) CITY: Atlanta
(D) STATE: Georgia
(E) COUNTRY: USA
(F) ZIP: 30303-1811

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Selby, Elizabeth
(B) REGISTRATION NUMBER: 38,298
(C) REFERENCE/DOCKET NUMBER: 22000.0061/P

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 404 688 0770
(B) TELEFAX: 404 688 9880

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 828 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAAAAAAAAT TACCATTTTT GGGNGAACCT TTNATANTTN GTTCCTAGAG GGNGAGTCAG 60

GGGTAAAAAA AACGATNAAG GGAGTTGNGG CGATTGGAGA AGCTATTATG AAGGGATAAA 120

ANACTTAGGT TGAGCCGGCG GGTGGGGTGT ATTCTTGGGG TGGNGAAAAG NNAGATCAAC 180

ATGAGATTTT TTTGTTTTAG GTTTTGCATG TTGTAATGCA ATANTTTAAC CTGATTTTAT 240

GTGCAGGATG CCTGAGGTTT GTGAGCAGGA ACACAGGAAA AGGAACACCG GTANTCGAAC 300

ACCGGTGAGT CCGCGCAGCC GCAGAGAAGG CGGGTATCAT TCGNTCCACC CTGTATGNTA 360

ATATGGAGCG CTACGGCCCC GCCCCTGGGG CCGATGGGCC CAAAAAGGTA GGGTTCGAGA 420

AGACGTCTGC ATGGAGCAGT GGACCAGTGA AGACCCAGGC AAGGCCGAAC GTTGGGCCCC 480

GGGCCCCGGG GGCGGGTAGC AGGGCCCATA CATTGTCCAA GGGCTGCTGG AGAGCCTGGA 540

GCCTCGCTCC CCCACCGGCG CAAAGTGGTA CAGCCCATGG GGGCGTGGCC CATATCATGG 600

ACGCGAGCGC GGCCGCCATC TTGNTCTGCG GTGCTGGTAT TTAGAGCGCA GCGCCTGACT 660

GGCGGGGTCG CCTTCGCATC CGCCGCTTCG AGAATCTTCT TTCGTCTGCT CGCTCTCTCT 720

CCCGTCGTCC TAGCCCGCCG CCGCCTGCTG AGCTTGCCCT CTTCCCCGCT TGCAGACATG 780

GNGGACATTG AAAGACCCTA CCTNAAGGGC CNGCANGCNA GAAAAAGT 828

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 845 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCNCCTAAGA NANGAGANAG GTTAGATGGN AATGGAGANT ANATACCGGG CTTAGCTTCG 60

CCNNGGACCC ACCNAGGGGA AAAGAGCCNT CNNGCAACAA ACNAAAGGAN CGGAAAGAGG 120

AAGGGNANGN GGNNAAACAN ATTGGGCGAA TTTAAAANCT NNGNCCNGTT TGAAATAGNG 180

CNCGGCCGNT CCNTGGGCCN GATCCANCCT TCCNTNACTT TTCNTCCCCN GCNTTAAATT 240

GCGNCGNCGG CCCCCCCAAC CATNTNTTCC GTTTTNANCA CCNGNGGCCC CGGCAGTGCN 300

GATGNNGGGG AATTGNNAAT GCCCCCCANC CATTTTGNNT CNGNNCCTGG GGAGAGANTN 360

AAACGGTGNG NGNAGNNGTT AATATGGCGG CAGCGGNGAC ANCAGTAGCC AGNGCAGGCA 420

CGCGNAGTTG GCNGGGGACG CCANGTGNCN GGAGANNTGG AGCGGCGGCG GAGCGGGCNC 480

CNAAAAAAAA AAANAANNGN TGGTAAGGGG GCCCGGGGTG GANGANATTT CNNGGGCNGC 540

TTCTAGGNGT CANGNTGNGG CCGCTNCGTT CGGCCCTGGA TGNAGCCCNG NGCCNGTGCC 600

NCCNCCGGGG GGAGTTTGTT TCCNTCTACC GTNCCCTGCT GNGGAGCGAC GANCTGCANT 660

CCCCNGGAGC GTCTANNAGG CCGTGGCNAA CCCCATCNAN GCNCNCCAGT NAGCTTCCTT 720

CNTCCCGACA TAGTAGGCGT CNGGNGGCGT TGNCGACAGN GGCCNNCGTC GATGGGANNN 780

TCTATTTNNG NTTCATGGGC CGTATGTTAG ACCTNTCGAA GGACGCGNNA AATAGATAGG 840

GGGGG 845

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 818 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TACACCTTTG NGNGTGTTGA AAATTACGGG GGANANGAAN AAAAANGTAT CCTTTTGGAN 60

GCCCCGGNCT CTTGTGGAAT TTGTGATTTA CGGCGGNANT CATATGATTT CGGAAANAAG 120

ATAAAGCCNN NCNNNNNGGG GTAGGGAAGA AGGATTTTGN AAACAAANTN TGGGTNTATA 180

TAANNGTGGG GGGGGGAGNT CATTGAGGNG GGGNGGAATA TNNAATNTTT TTTTTTTNNT 240

TNNNNGGCAA GAGGGATGAA GGTAAGGTTA GTATGAAATG GCCNNNCCAG AGAAGTTNGA 300

TGAAAAAGAT AGTGCCACCA AGAGANATNA TTTGTTATTT TTAACAGTGG GGGGAGGTAG 360

TTNTAGACCA CCATTTATTA NAACTGAGGC ACAAAGAAGA TGATTGGGGG GCACTTACAG 420

AGTAAGCAGT ATTTACATAA AGATTTNTTC CCCAGGAATN ANGAGGAAGN TGGATAACTG 480

AACAAAGCCA TGTAAGCAGG CTTTTTGGTA TGCATGTGGT CCCATTACAA GGAATACCCA 540

ATAAATAGCA AATGCACACT GCCATTCACA AGCAATTGCA GAGAATGGGT GGGGGATGTG 600

AAACTAAAGA GCTTTGTAGC TGCCTGAGGA GGTGGGTTCT CTATATCCGT GGGAGCTAGT 660

GATCCCCCAC AGGTCTTAGC TGGTGCCATG ATTGTGATCT TAGGCCAGAT TTGATGTCCC 720

CCACATGGCC GAGTCCGCCA TGGATGCAAC AGGGCAGCTT TATTTGCTGT GGGCNGGTAN 780

TGAAGGATNT CACAAATGAA CTTGGCAAGT AGAGAGGT 818

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 857 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGGAAAGANT GNGNTAAAGT TNAGTTNNNA GATATTGANN AANNTNGGGN AAAANAAGGT 60

GNNNNACAAT CTCNCAANNA TTTNAANGAA GGGGGAATAA ATGNAAANTG GGANTTAAAA 120

AAANAGGGGN NANANGNTTN NGGTTNAANA NAAGGGGGGT NTNCCCGTTT TTTTTTTAGG 180

ATCCTGGGAG TAACCNACAG GAACCNAAAA TTNGNANAAG GGNGNTCCTT CCCTTCCNGT 240

CAGTAAGGGA TGGGGCCCTA TTTTTANCAA CGAACACCAT TGACAGGANA CCGGTCAGNA 300

TTCCGTTAAG TATTTTGACC TTTCCAGGGG ATGTNTCCGC ACAGCCGTTG NGACCTTAAA 360

CGCGNCCAGA TTNTGCGAAN GTCATTTTGG GAATGACTGT TGTAGACACT GCTTTTTTAG 420

TCGCAGATNT GACCGCAGAT TTTCNTTTCC CACCTTATGT CCGNTGGAGC AGTGGTGGCC 480

GGAGAAAATT TCTTGGGGTT CCNTCCCGNG ACCCAAAGAA CACAACTGTT CTCGCTGCCC 540

GGCACCCATC GCCACGTCAG CTCACGCTCG CGACGCCAGC ACGCNTGCGC GCAGAGAAAG 600

GCGGAGCATG CGCAAAGGCC TGCNTNTAAC ATCCGGGGCT CGGGCGGCGG CGCTGCCGCC 660

GCGAGGGATT AANGGGGTCT TTCNTTTCNG TCTCTGGCCG GCTGGGCGCG GGCGACTGCT 720

GGCGAGGCGC GTGGAAGCTC GCGATAGTTC CCCTCCGCCT CCTCTTCCCG GTCCAGGCCA 780

CTAGGGAGTT CGCTGACGCC GGGTGAACTG AGCGTACCGC CTGAAAGACC CCACAAGTAG 840

GTTTGGCAAG TAGAAAG 857

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 896 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGGAGAAAGG GGCGACNTTT ATTGGTCCNG GAGNGGGGGG NCAAATGGGT TTTTATCCAN 60

TTTAACGGGG GGAGGCCCCG GNNGAGGAAT TCCCGGGGGA GGAANAAAAA CAAGATCCGC 120

NTAAGAGGGN GGGGGTNTCC GNNNTTNTTN GAATNGTGGN GCACCGGGGG GGCAAGGAAG 180

AGGGTTCCCG GAGAATGGGG NGGATAAAAN GATTGGCAAC TCACCCCGGN TAGTTGTACC 240

AGGTGTTTTT TTTTTTTTTT TTTGTTCANA AANAGGAAAA TGATTCAAGT TAAAAAAGTA 300

ATTGGCAAGG AAATTTTTTT CCTANCCTCC TTGAAAAATA GTGGGAACAG GGGTTCCCAA 360

GGGGAAAGGT CCCCNATTNA ACAAAATGNG TTTCAGNGGA GTGTGGCCCA CCCATTGTGT 420

NTCCATGGAA GAGTGGCTTT TNTGGNGAAG TTCATTTTCC TTAACCTTNA NNACTGTAAN 480

GGNTCTTGTG CTTGAGAATA TTGTTGGCCA GCTTTATNGT CTTCATTTNT AANACTATTT 540

AGACTAGAGT GTTNTAGATT NTAGGTCTTC ANGTTTCCAG TCACCAGTCC TTGGCTTTTT 600

AGTATGGAAA TCACCAGTAA TGGCAATATA ACATCCCTGC TTCTGTTTCT TAGAAGGCTN 660

NATTACAGTG TGTTCAAACT CCGTGTCATT GCAACAGGTT AAACTAACTT TNTACGTAGG 720

ACATCAGGGT ATTGACATTC TCATCCTAAA GTCAGTTTGT CTGTTTCCAG AGGAGGAACT 780

GAAGCAGTGG TTCTTTAAGT AACTGACTCA GGGCTTTCCT GCCTGGCGCG CCTGCCAGGC 840

ATNGTGTAGC ATTGTACTGC ATCTTCTTTG ACCAGTTTCC CCAGGTGAAG AGCCTG 896

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 937 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGGCCCCCCC CCCCCNANTT AATTTTNGGG AAGAAAAAAG GGAAAAAANT TTGGGGTCAG 60

GAAAAANGAA GTTGGNAANC GNNGGGGNGN CAGNATTNGA ANAGTGGGGG ANNTTAATTT 120

NAGAGGTCCC TTNNTTCCNN GGAAAAGTTT AAAAGGGGTT CAATTAACTT NGGATCNCCA 180

TTTATCAGAT TACCCGNGNG TCACCTGGGG ACCCTTTACN GGTGGCGGGA CATTNGAAAN 240

ACATATTAGT CAGATTATAC ATAGCAAANA TAGTTAGGAG CACAANGAAT CATTTATGGT 300

GGNGGTCACC ACACAGGAGA TGTATTATCC GCAGTATTAG AGAGTTGAGA ACCATATNTT 360

AGAGATGCGG TAGACTGACT GTTCCCTTTT CGNTTGGAGT GACCTTGCCA TTAGAGGCAA 420

CAGCATCAGT ATTGTTCCCA GTCCCCNTCA CACTGATTCG AACTTTAAGG ACACTGATCT 480

NTGGCTGGTA GAGGTTCAGC ACACATACCA GAGTTACGAG TCACGTGCCA GAAGGGCAAA 540

CTGAACACGG AATTAGAGGG AACTCGATGT CTCCGGCTTG CACTGGTCTT CTCTTGCANT 600

AGAATCCTTC ATCCTGCTCC CAGTCCGGAC GTCCAGGCAA CAAGGGCGTG GAAAGTGAGG 660

GGGCTGGGAG GTGTGTTTGC CTTGCCTCAG GCGNTGGGTG GGGTTGGGGC GTGCCAGCAC 720

TCCCCTGGGC GGGCNTCACC GATGCTGGCC ACTATAAGGC CAGCCAGACT GCGACACAGT 780

CCATCCCCTC GACCACTCTT TTGGCGCTTC ATTGTCGACG TGTGGTGAGC TCTCACTGGG 840

GCGTCCCTCT AAGATCTGTC CACTNCCTGG TCTAGGGGTT AAGCNTTTTC CTGCCCTGAA 900

AGACCCCACA ATGTAGNTTT GGCAAGCTAG CAAAGGT 937

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAAAGGGGGC CCCAGCGGNG GGGGGTTGTC CAAGGAATCA AAANGTGGGG NGGGGGGGAA 60

AAAANTACTT TTAAAAAAGG CNGCCNNANA ATANANGACG TTCNGGGGNG TTTGAAAAAA 120

GGCCGGAAGC CTCGGACNGG TTTCNNTGTT AGGACAAGGA AAAAGGGNAC GCACNGGGAT 180

TTCCTTTCCT TATNTTAGCA AATNGCCGGC CAGGAAACCA NCGAGTTGGG NGGGNTTNGG 240

TTTTCNGTNA AAGGAAAGCA GGGGGGGGAN AAACACGGAN AAAAAGGGAA GAANNGGGTT 300

NATTNNGGTT AGNAATTGGN TCCCAGAGAG NGCCAAGAAA ATNGGCCTGT CCAAAATTCT 360

TTTTCCCNGC TTTTAAGACA GGCANGATAN TATNNGGCAG CAGGTNATTA CCANAGGTAA 420

GTAAATTACA ATGGGTAAGG GCTTGGCACA GGCCAGGGTA AGTAGGGCAN GTATGGATGT 480

TAAACATTAC CCTTCATCCN GAGGNAGTTA ACACAAGCAT TCNTGGCGGG TCTCACATAT 540

CCCAAANAAA AATNTTCAAA AGNAGCCCCN TGGGGAACGT TAAGCCAAGC NTANGACTCA 600

CAAGGGANGA CATGGGCAGG NTAGGGNACA GAATCAGTGN TCAGAGACTC CAGGGGCACC 660

CCTGATTCCN TTTGNTGTCA CACAGACANT GCTCCAGGGA CAACCTTCCC GGANGTGAGT 720

ATANGACTTT CCTGATGGNG ACGCTGCCGT GANGGGACAC TNCCTCGTGG TAGCACACAT 780

TCCTCAGTCA GCTTCTGAGC CTCAGGGTCC CAGCAGGCAC AGTGGCAANG ACCTCATTCT 840

TCTCGTCTGT CCCACTGAAA GACNNTCACN AAGGAGCTGG CTAGTAGA 888

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 980 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGAAATGAAA AAGAAGGAAA GCTAAAAATA GATTATAAGT GTTCTATTTG AAAAAAGAAA 60

GAAAAAAAAG AAAAAGAACA CAGAGAAGAA TAAAGGAGAA GAAAAAGGAA GAGAAAAAAA 120

AGAAAGAAAA AACGGAAAAG AAACCTAGAA AATAAAAAAA CAAAGTATCC GATAAGGAAG 180

AGAAAGGAGA AAGACTTACC TAGAGCCCAG AAATAGAGAA ACTAGAACAA AAAATGGAGA 240

AGAAGAGGAG AGAAAAAGGA TTAGAGAGGG TGAGGTAGAA GGAAGAAAAG ACAAGAAAGC 300

AGAAAAAAAC TAACAAAGAT GCATATAAAC AGAGAGAAGA TGATTAAGAT TAGAGAAAAA 360

GACCAAAGAG AGAAGGTAGA CAGGACAAAT AAAACAAAAA CAGGAGGGGA GAAGGGGAAA 420

GAAGAAAGAG GGCAAAAGCA AAGGAATAAG ATAATAGCAC CAATAGCAGG ACAGTAAAGG 480

GTAGAGAAGG GACCATTCCC TACCCCATAG GGGGGAACGA CCCCGGAATC AAAATACAAG 540

GCACCGAGCT GAACCTGGTT ATCACACAGG CAGGAGTGGT ATAGCACGGC GTTCCGGGCA 600

AAAAAAAAAA TGAAAAATAA ATTCCTTCGG GCGGAGAACT AGAAGAGGAT GGGAACTCCT 660

TGACAGAAGT AGCAGGCAGG AAGCCAGCCA GCACCCCAGC CCAAACAGAA GCAGCCGCAA 720

TGAAACGGGC GGCAGATCCA CATCCGCAAA GTCCTCAAGG GAGCATCGGC GAGGCCCGGA 780

GCCAATGAGG AAGGGCAGGA AACCATATCA AGCCGAGCGT CGGGACGGCT GCCATGAGAC 840

ACCCGGAGAG GTAATTTTTT TTTTACGGGA AGCGTCCAGC CAAGTTAGTG GGCCGGAAGC 900

GACGGTACTT TAGTATACAT CGTTTTGCCC GAGTGGTCAG ATTCTTTTGT TATCCCCAAC 960

AGAACCGTAA GCTAGAAATA 980

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 845 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TCNCCTAAGA NANGAGANAG GTTAGATGGN AATGGAGANT ANATACCGGG CTTAGCTTCG 60

CCNNGGACCC ACCNAGGGGA AAAGAGCCNT CNNGCAACAA ACNAAAGGAN CGGAAAGAGG 120

AAGGGNANGN GGNNAAACAN ATTGGGCGAA TTTAAAANCT NNGNCCNGTT TGAAATAGNG 180

CNCGGCCGNT CCNTGGGCCN GATCCANCCT TCCNTNACTT TTCNTCCCCN GCNTTAAATT 240

GCGNCGNCGG CCCCCCCAAC CATNTNTTCC GTTTTNANCA CCNGNGGCCC CGGCAGTGCN 300

GATGNNGGGG AATTGNNAAT GCCCCCCANC CATTTTGNNT CNGNNCCTGG GGAGAGANTN 360

AAACGGTGNG NGNAGNNGTT AATATGGCGG CAGCGGNGAC ANCAGTAGCC AGNGCAGGCA 420

CGCGNAGTTG GCNGGGGACG CCANGTGNCN GGAGANNTGG AGCGGCGGCG GAGCGGGCNC 480

CNAAAAAAAA AAANAANNGN TGGTAAGGGG GCCCGGGGTG GANGANATTT CNNGGGCNGC 540

TTCTAGGNGT CANGNTGNGG CCGCTNCGTT CGGCCCTGGA TGNAGCCCNG NGCCNGTGCC 600

NCCNCCGGGG GGAGTTTGTT TCCNTCTACC GTNCCCTGCT GNGGAGCGAC GANCTGCANT 660

CCCCNGGAGC GTCTANNAGG CCGTGGCNAA CCCCATCNAN GCNCNCCAGT NAGCTTCCTT 720

CNTCCCGACA TAGTAGGCGT CNGGNGGCGT TGNCGACAGN GGCCNNCGTC GATGGGANNN 780

TCTATTTNNG NTTCATGGGC CGTATGTTAG ACCTNTCGAA GGACGCGNNA AATAGATAGG 840

GGGGG 845

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 528 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGATTTNNTA ACCTTTCNGG GAAGGGNGNG GAAAAGGNGC CAAACAAAAA GACCCCNNTG 60

CCCGGAAATN CTTGGGGGNN ATTGNGGAGC GTTTTTTANN GGGGATTGGG GGGNTNGGGN 120

TGCNCCCNNA TATTCCCGGC TNAGGGGCAA CCCGAGGGGT NNTNTCCGAC CATGTAACTT 180

GTTTCGGAAT GAGGGGGAAT GCNNATTNTG ANTATTGAAN NGNGACCCGG NGGGGNCNTG 240

TTNNAATTAA CCTNNTACCC GGAATTTCNG CGAGANCGNG ANGATNNCTG GCACTTNTTC 300

CGTATTACGN GTGGCGTTCN NGANTGCAGG GGNTGCCCTT GTTTGNNTTT CTGAGGGTTT 360

CTTATANGCA GATTGTGGGG TTGGAAACGA GANATCCCTN ANGTAATGCC ANNTCACACG 420

GGATGGAGCA GGAACNCCCT ACGNATAGTT NACCTTCANT CAGGGTGGGG AANCGATNGA 480

CCNGAGGTAT ATGGGCNGAA CNGGACATGT NGGGNNANCC GTTCAATC 528

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 927 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AANACGGTTT AATAAGGGGG ATGTTCAAAA CNCCACTCCG GGGGAANAAA ANAAAAAATT 60

AGGGGGGGAG AANGGATTGG NGTATAGTTT CCCACCACAA ACCTNGTTCC ATTTTTTCGG 120

GGGGGNAACG GAGGNCATGA TTATGGGGTG AAGGCAGCAC CCACCCATTT TTCGGGGGNA 180

AGTCAGTTTT TTTTGGTANA ATCAAAGTTC CTTCGAACAT NTCGTTTTAT CCAAGGAGTT 240

TTGGTGTTAA ATTAGCANTT TNTGNGAGTT TCAAAGTTNT GGTTCCNGAG NAGNTTTGTA 300

ATTGGTTCAC CGGTTNTTTT GNGCCAGGAA AGCAGACCCN TGTTNGGAGG GGAGATTCCN 360

ATTTTTAGTT CCCATTTGGT GTTTCCNTAG GTAATGGAGT CTGCAGACAG TTTGAGTNTA 420

NTGAGTTGAG TCCCTTNTCC TATCAGCCGG GGTGGCATTC TGTCCAAAGG AGGAATCCAG 480

CAGCCAGATT AGATTTCAGT NTCNTTTNTA ACAGGGAAGT TAGACACACC CGGCCAGNTT 540

GCAGCCTTTC CACCCCCAAN GAGTGAACCC TGCCNTTTCA GCTTTTACCC AATTTACTTT 600

CGTTGGCTTA GCATGCAGAT TNTTTGGCTC CATGCCCGGA GCAGCTGACA TGGGAGGCTT 660

TGAAACTTCC ATTATCATAG AATGGCAGGC AGGTCCTTTG CGGTTAAAAC CAGGAGCCTG 720

GGCCNAATGA GATGGNTCAN TGAGCAAAGG CGNTTACTGC CAACCCTGAT GCCTTCAGTT 780

TAGTNTTGGA ATTCACAGGG TAGAAGTTGA ANACNTTTGA CTCTTCAAAA GTTGTCCCTG 840

TAGCAGGGCA GNNGTGGTGC ATNCCTTTAA TTTGGGCTAC TTTGTGAAAG ATATCCACAA 900

NGAACCTTGG CAAGTAGAGG ANGTCGT 927

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 911 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGGAGTTTGC TCTCAGAGNG CCNATTACGC NACAGGGGGN GTCTCACANT ATAANCTCAT 60

ATANNATACT CTACNNTNCC CCCCCTNANG TNTCAAGGGC AAGAGAATAT NNTCTCTCTC 120

NTATCGTCTN GGGGNNTCTN AAATGTTTGN GCTCCCCGGG NAAAATANNT CTCTNTCNCG 180

NCTCTATNTT CTCNCCTCAC ATATNTGCGN ACTCTTTCTC NNCCACANNA AAAGCGCCCA 240

GTGNGGGGAN CTCNNAGAGT GTATNGNGAA GAACTGNNAG TGTNTNTGGG GCGCGTTCTC 300

GGGGAGANNA TACNCTTCTC TCNTCTCTCT NTAGAGTGNG ATGTANAAAA CCNCANNTGT 360

TGCANAGANA AATGGGGCTC NGAGNCTCTT ATATTTCCCC NCCCCTCTCN CCATATATNA 420

CCTNCGGGGG CTTNTNTNTA AATCNCCTNT CNCCATTNTT NNNANNNGCG TGTTTNTATT 480

GTNNGTNTCC NCNTGNTCCA AAAATCTCAA ATTTGTGTCT CTTNTCCCAA ACNCTATNTC 540

TCCCNTANCC CTGGGGGNGT NTATTATNTN TNTNTATATN CNTATNTTAT ATACNTATAN 600

TNTATNTNNT ATATATTTGG GGTCNTTACC AAAACCCCNT TTTTNTCTCA CTTTTCNTCN 660

ACTCCCTTCC CGGGGCCTNG AAANTTTATT NCCNNCCNTT NNGNTCCTTT TCTNTTAAAT 720

TCNTTNCNTN NGGAAAACCC TTTTCNAAAC NGGNTTTCCC CTTTTNNCNT CCCNCTCAAA 780

CCCCCCAAAT TNGGGCATTT TTTCTTTTCC CCTCACCNAA CCCCNTTTNC CTCCCCCCNC 840

CCCCCCCAAA NTGNGAATAC CCTGNTTTTC AGNGGNNNNG AAAAATCCCT CCCCGANGGN 900

GCCCCCCTCC T 911

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 880 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGGCACCAAC GGNGGAAGAG TTTTCCANGG TANAAGAAAG NAGGANTGGG NCGANAANAA 60

TTANTTTTNA AAAAGGNCAC CAGATANAAA AAACTTTTNA GGGGNGTTAA NAAAAANGCN 120

GAAACCCTCN GACGGTTTTC NNGANTNTTA AANAGATTCA GGGGAAGCAC GAGATTATCT 180

TTTCNTTTTT GAGCAAATTG CCAGCAGGGA ACNGACNAGA GGNTNGGTTT TTGNATNCNN 240

TTAAACGTAA CGCAGNTTTG GANAAACACA GNTNACATGG AAAGACCTGG GNNATTAGGG 300

TAANGNAAGN GGTTCAAGAG AGAGCCGATG AAATNGCCNG GTCCAAAATC TTTTTCCTTG 360

NCTTTAANAC AGGTNNNAAA AATNNGGCTG CTGTTTATAA CNATAGNTAA GTGAANNACA 420

ANGGGTAAGT GNTTGGCACA GNCCAGGGTA AGTAGGCATN NAAGGAATGT TAAACATNAC 480

CNTTGATCGN GNGGTTGTTT ACACCGCNTT AAAGAAANGT TTAAAAATAT CCCTGGGCTG 540

TTTCTTCCTN GGTGCCNCAN GGNGAACGAC AAGCCAAGCG NATGANTCAC AGGAGACGAC 600

ATGGGCAGGT TGGGTACAGA ATCAGTGTTC AGAGACTCCA GGGGCACCCA GATTCCNTCA 660

GNCTGTCACA CAGACACTGC TCCCAGGGAC AACCCTCCGG GATGTGAGGN NANGACTTCC 720

GNGNNGGAGA CGCTNCAGNG ANGGGACACT CCTGGTGGTA GCACACATTC TTCAGTCNGA 780

TTNTGAGCNT CTGGTCCCNG CAGAGNACAG TGGNAATGAC TTTTTTCTTA CTTGNGNCTC 840

CAAGGGCGTC TCCACAAGAC AGCGTGNCNA GTAGATAAGT 880

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 923 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGGAGGAGTA CNGGANGGGT CCGACGTAAN TNTNTCACAG GNAAGNCGAN ANGAGGAGGG 60

GTNGCGTAGG NNACAAAGAG ATAGGAACGG GGNCGNNAAC NTNNCNTNTN GAAAAGGCCG 120

CCANNGTNAA NCAACTNTGG CGGGGGTGGG ACNNAAGGCG NGNGGCNNNA GAAGGTTTNN 180

TTNNTTGNAA CCNAGATTCG AGGGACGGAC NGGANTATCN TATCCNTNTT NGTTNCGANT 240

GCCNGCGNGN ATCNGGCNAG GGAGGGTNGG TTNNNNGGTT TCNGGNGACN NCCCCAGTTT 300

NTGGNNNATA CCCNGCTCTC ACANGNNGGA CGNGGGTNTT TNNGGTGAGG AAGNNGCNTC 360

CCCGCGAGAG CCCGNGGNAA GGGCGNGTCC AAAANTCTTN TTCCCTGCTT NTNCNACAGG 420

CTNNGANANN ATNNGGCTGN TGTTNATCNC NATAGGTAGN TCAACCNNCA NGGGGANGTG 480

CTNNCACACC CCAGGTTAGT GTCCCNTNCA NGGTATGTTA ANACGTTACC NNTGATCGGG 540

GGTTNTTTAC NNAAAANNAA AAAAAAANTC ACCNTCCCGG GCNTGNTGNT TCCTNGGGGC 600

CCCANGGTGA ACGACNANCC AANCTNTTGA NTNACAAGGG ACGACGTGNG CAGGTTGNCG 660

TNCNGAGTCA GTGTTCAGAG ANTTCNGGGG CACCCCTGAT TCCCNCGGNN GTNACACAGA 720

NACTGNTCCA GGNNCNNCCC TCCGGTTGNG AGTCNAAGAC TTCNGGNNGG TGACNCTACN 780

GTGANNGGAC ACTTCGTGGN GGTGNCNCAC ATTCGTCGGT CGGCTTANGA NCNTCTNGGT 840

CCCNGCAGAG CACTNTNGCA ATGNCTTTNT TTGTTCTGGG GCTTCCNAAT GGGTCCTCCC 900

AAAAGNCNGC TTTAGCTGTA ATA 923

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 880 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ANANAGAGTA ANTAANANAA GAGGAAGAGA NAAGAAAGNA GAAGGNAAGG ANANAAANGG 60

GNNGGCGAGG AAAAAAGGAA AGGAGAANAA TAAAAGAAAA AGTGAGGAAG GAAGGAGTAN 120

NAGAAAAAAG NAAAGNGGAG ATAGNAGAAA GGNCCGGNGG ANAAAAGANT AGATTAANGA 180

NAGNTGAAAG AATAAAGANN ANGGCGANAA GGAAAGAAGA NCGAGNATTA GAAANAAGAG 240

AGGAAAGANN NGGGGGGAGG GAANGAGGCG AANTCNNGAG ANCAGTNNAN AAGGCAAGAG 300

AATNAGGAGN AGANANGAAG NNNANGANGA AGGAGGGGAA AGAGGGNACA GAAAAAACAA 360

GTANAGTAAC CNACNNCNGC GAGNGNGCCA AATAGGTNGC GCCAGCNACA NGGCCCGAGC 420

CCNGGGCGAG GGGGCATCAN GAGCCAAGGG GAGCGGGTCC AGNCNTAGTT NTGAAAGGAA 480

AGGGGAGGNG GGNAGATATT ATATGGTCGN GCCCCCCCCN GTGTCTCGGT GAAAAAAAAA 540

AGGNGTGANN AGCAGGGCCN TNTTGGNTGN GGGATCGNGC ATGATCAGAG ACCNGAGGCC 600

GGACNTTCCG CNGNGCCTTC CGTAGGCCCA NTGTCAAATG TATTCAAGCC GGTTNGAAGG 660

ATGCCGGNGN TAGNGANTGA TGCGGGGGCC NGCCCCCCCG GNTTTCCGCC CCCGCAGCCN 720

CNGTGGCCGC CATNACGGAG TTCCCAGTGG TGAGNGTGCG GAGNTGAGGC CCCGCGGGTC 780

GCCGCCGGTC CCCGCAGACA GGAACGCGGA GCGNNCCCTG CGCTNGAACG TANGGGNCCA 840

CTTGAAAGAC TNNACNAAAN GACGCNGATT TGTAGAAAAG 880

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATTCTTCAGC TTTTGCNTAG AGGAAAAAGA ATGGATTGTT TCTAGGACAA CCTGCTGAGG 60

TGCTCACCNA GNGTTCTCTC TCTCTCTCTC TCTCTCTCTC TCTCTCTCTC TCTCTCTCTC 120

TNTGNCTCTC TCCTGAANNT CCCCANAGGN NCTTNGCAGN AAAANG 166

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CNTTTTNCTG CNAAGNNCCT NTGGGGANNT TCAGGAGAGA GNCANAGAGA GAGAGAGAGA 60

GAGAGAGAGA GAGAGAGAGA GAGAGAGAGA GAACNCTNGG TGAGCACCTC AGCAGGTTGT 120

CCTAGAAACA ATCCATTCTT TTTCCTCTAN GCAAAAGCTG AA 162

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 871 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAATAAAACC CCAGAAAGGT TTTAAAACAT TCCGTATAGA AGTTGATNAA TTNAAATAAT 60

TGGAGGTGAA ATACACAGAG GGTTTTTCAA TTAATCAATA AAAAAATAAA TTACNTACNT 120

NTTTTGGGGG GTTTTATGNA NAAANGAATT GGAGGGATCA ATTTGCAAGA AATTTATTTT 180

TTNGTATTAT TTAAAAACCG TTANGGATTC NGTTGATTTT AAATCAAGCA GTAAATATAT 240

TAAAAGGTAG GAGAATGGTA TCAATAGGCC AAGATAACAG AGTGTAAAAG TTAAAAGTAT 300

TGGACAGAAA TATTAAGAGT TATTGTTAAG ATCCNGGACT TTGGAAAATT TAAAACCAAG 360

CGATTTAGGC CAAGTTATTT CCACAGTATG GTATCAGAAG GAGTAAAGAG ACAGCACAGG 420

TGCAGATNTG ACGGCTTGGT TCCTTAGGTT ATTGCCACAG CAACGGTCTT GGCCGCAAGG 480

CAGGCTTGGG CCCAGCATGA GAAGAGAGGG GGAACCAAGT TCTTCAGGGA CCNGACGGGC 540

GGCGCCGGTG AGAAAGGACT TCATCTTGCC ATGNTCANTC AGCGAAACTG CAAACGCTTN 600

TGGCAGAGAC AACGCCAGAT CTGCAGAGGC ATTCCGGCCT TTAACCGCTT TCCCACAGTC 660

GGCCCACAGG CCTTACCGCA GCAGAAAGCG CGCGACCCGG AGGTCCCGCC AGTCAAAAGA 720

AAAAGGGGGG CGCAAAACCA TATAAGGCNT GGAGCAGGCG GCCCGGCCCC GCCCCCAGGA 780

CATGGGCCCG GCCCCAATCA TGCCCCGCCC CCAGGATTCG GTCCCGCCTC CTCCCGCTCC 840

CGGGATGGGC CGTTATGCTC CCGATACGCA T 871

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 936 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TGGGATTCAA AAATTGGAAG TTANTTTTTN AGGAAATTTN TTTTTAAAAT TNTAATTGGG 60

GGGNNTNGCC ACCAATTAAA ANGNGTTTGA ATTNAAAANG ATTGCCGGGG GAAAAANCCA 120

TTTNCTGCAN GGAATTAACC AAGTAATTTG GNTTGGNAGC ACTNGTTTTG GGCCTNTAAA 180

AGGCATTTTA AANACAAATT AACAGGGCNG GCATNTTCAA CGGGNGNTAG NTTGTTTTNA 240

TGAAACNGAG GNTTTTGGGG GCGGGCCTTT CCNATTNGTT TCCTTTTTTA GGATTAACAG 300

ATGNGAAAAA AAATNATGGT TTTATATCAT CGTTNTTGGC ATCAGCAGAT TGGCNATTCA 360

ATTAAAACAG ATCATTCATG ATNGGCTTTT TGGCCATTAC CATGNAAACA CAAAGAGCCA 420

GGGTTTGATT GCCCTGACCC GCCNACCTTC GGTTGCTTAG GTGAGGTGCA GCACTGCGTT 480

TTTCCTTTTC GGACTGAAAA CAGGCGAATG AATCATTTCN GTCGTGTCTT GAGGGTGCAT 540

TTTTNACATT TTTGTGCCNT GCTGTGCGCC GGTGTGTGAT TTCCCTGTTT TAAGTGGCCC 600

CTGAGGATAA CAGTGAAGTG CTGTCTAGCA TTCTTCTGCG CAGGAAGGCG GAGATCTGCC 660

CTGCGGAGAA AGTATGCGTG CTGGATAAGC ATTACTGAGC ATGACACAGA GCACCGTTGA 720

CCCCGAGTGC AGCGTTAGTG AACCGGCCAA TGTGCTGGGG GATTTTAAAT GGAATCACAC 780

AGAAGCTGAG GCTGAGGATT GATCTGTGAG TAACAAGTTG TGAATGAGGC TGGCAGGAGC 840

TAGCCTGGGA GTAAGATTCA GTGTTTGNTA ACAGCGTGCA GGCATTAAGC CAGGGAACTG 900

AAAGTNCCCA CANNGNCTTT GGCAAGTAAG AAGTCG 936

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AGGNNGGGGG GGGAAACTTN TTTATNTGGA AAANTTTTGT TTNGGCGGGN AAGGAGTTTT 60

TAANAANGTT AANGGAAAAA GCTTTTANTT AANATGACCT TTTTGGGGGA AANACAAANT 120

TGGTNNGTGT ATTNGNGAAA AAGATTTATT ATAAGATTTT TTATAANATT TTNGGGGGGG 180

AAATATTTCA AANAAAATTC TGTAACAAAA GGNTTTTTGT TTTTTGTTNT CCAAGNAGTT 240

NTCCAGGTAG TTNTCAACAA CNNANGCCNT AGGGAAGGAC ATCATATGGA TATTTTCANA 300

GATTTGTTTT TAGGAAACAT TNTAAAGTCA AGGTTAAGAT GACAGTCAAN TCCCANGAGN 360

GNGGTAACTG TNTGCTTCTT TATTTAAAAT TCAATATTCA GGATTTCATT TATACTAACA 420

AGANTAATTA CCATCTTAAT GAAACATAAT TTGAATAATT TGCAAACAAT NTGATTTTTC 480

TTGAATATAC ATGTTACTAA AATATTANGG ATGCAAATAG NTAATAAACA AATAGATANG 540

NAACCATGGN ACACCCCTTC TGTGATTGGN GGGACNTGGG CATAAGGCTT GTTTGTATAA 600

TAATGTTCAT ATTTTACATT CTTCCTNNGA GGANGGTCCT CCCTGTTAAG AAAANGACTC 660

CAGGATAAGG AGACAGCACC AGTNTAGGAA GTGAGGNTCT GTTTAATGTC TTAGCAAAGT 720

AGTAAATGNT GGGACCATCA GAATAGCCCN TAAGGNTGTG GANAGAACTC TAAAAGCNTG 780

ATATATATAT ATATATATAT ATATATATAT ATATATATAT ATATATNTAT ATAAAGAGGC 840

AGTATTGAAA GACNTNCACC AATNGAGCTG GCNAGCTAGA AGAGGTCG 888

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CTTGGAAGGT TTTTTTNNCA AAANCCNGGG NGGGTTTTTT TTAANAAANA GGNGAAAAGA 60

TTTGGAAACT TTTTTTTTTG GTTGAAGTTA NTTGGGGATT GGGGGAAAAA TTAAAAGGAT 120

TCAAAGTTCC CATGGNTTGG AAGTANAACT TTTATTCAGA AGNGAAAGTT TTAATAATGA 180

AANATGTTTT TTTGGATTNA CGGNGGNGGA ATTGGGGAGN GGAGAGAGAA GAGAGAGAGA 240

GAGGGAGAGA GAGCCGGATC CGCANTCGGG GGTTTCTACC GGCAGAGCCA GGACGGAGAG 300

GGTTTTCGGC AGCCGCNGCG GGTTCGGAGN TTTTAAGGTT TNTTAATCTT GGAAGGTGTC 360

TGANATNACC CCGTTTCTTG TCGGTGATGT TTNGTACAAG CTTTCATTTC TTCAGGATTT 420

CGGAGCGCCA ATTACTGCCC CGATNTGGTG TTTATGTTTG CCCGTTCNTG CGCNTGGCCC 480

CGCGCCCGCC CGNGAGCTGC GTTTTCCCTG GCCGCGCGGC CCGAGGGGGT GGGTGGGGGG 540

CCTTGGCCCG CGCACCCCAG CGCAAGGGAG GGGTCCCCTT CATTTTTTTT CATTGACTTC 600

AGCACCATGT GATCAGGAAG TCTGGCTCCN TCCATTTCCC NTCCCGACTG AAGGGAAACA 660

TTGTGTAGCA GCCCGCCGCG GCCACTGGTG GGATGGCNTT CGCTGGCCTG ANGTAGGGGG 720

ATAAAAATAA CCGGCATATT TAAGGCCGGA GCAGGAATCC CGGCGCTCAC ACGCGGCCTG 780

GTCAGTTCCC GAAGCCGCCA GCAGCGCTCT GCGCAGCGAG CTGCTGCTGC GCCAGCCAGN 840

TCGGGAGTGC GGACACCGTG AAAGACCTTC ACCTATAGNG CNTGGCAAGC TAGAAGAGGT 900

CGT 903

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 918 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TCGGGGGCAG GAAAANTTTG GGGTTTTCGN AAAAAAAAAA ANGGGCANAA ACCCGGTNAA 60

CNTATTNGTT TTNGGCCCNG AAAGTAAANA ATTTTTTTTT NAAAANATGG AAAAATTGAA 120

AAGGGANANG CAGGGAAGGG NGGNATTTTA TNTCCAANTT TCNGGTTCCT ACTTTTTTCC 180

NGATTCTGTC AGTTTCGCTT TAAGCAAAGG NGANGAAGGG NNAGTTTCAG AAGTTAGGCT 240

TGCCTGAGAA AATTTCAATG GGTGGCAATT CTTAGGACTC AGGACAGGAT TCAGNGNGGA 300

CTAATNTGCA TTTNGGGATN TGTCCCTGGG GTCCNTAAGN TCCGGACCGG GANAGATGTT 360

CNAGGGGGAG ACCCAANTAA CCCAAAGGAC TGAAATTATC ATGGCAGCNA CNNACCAGTA 420

GTTGNTCTGG TAATAGAGCA GATTGCTCAN AAACACGGTT GTTCCATTTG GATATATCCN 480

TGAAGTCCGG CCGTGCGAAA CGATCAGAGC CCGGGAAGAA ATCATCCCAG GCACGGAGCG 540

GGGCAAGGTT TAACGTCCAT GTTCTTTTGC TTGGCGAGCT TCGCCTTCGG AATCCGGAGG 600

CGGCGGCGGT AGCAACCAGC TGAATGAAAG ATGACAGCGG CTCNTTCGGA TTGGCTCTGC 660

GGTTAGAGCA CCGCAGGGCC CAGAAAATTG GCCGCGGGCG GGTGTGTTGG TCTTTCTGTG 720

ATTGGCTGGA AGTGGTTAGT GACGGAAAAC TGTGGGCTTT ACCAAATGTA AAACGGAGTA 780

CTAACAAAAA GTAACCAGCG GAAATGCCCC CCTAAACTAA AGGTGGTGTC AGTAGTCTCT 840

CTGGCAGTTT AAATACAAAC NATCTCTTTT TAGGCATTGT TTTGAAAGTC CCCACAAGGN 900

TTTGCAAGTA ANAAGTCG 918

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AGAGAGGGTT TAGCACAGGC AGCNTATTCC CAGTTTGTGC TGTAGAACTG GAACCTCAGG 60

CCTCATTCTG AAATNTGCAG CCNTCCCCAG CATCCTTCNT GGCACAGCNT GGCACAGACN 120

TGNTAAGTGT CTATTAGTGA CTAATACAAA GGAGTATTTC AGAACGTTGG CACATCTCAG 180

CACGTTGCAA CTGGCTGGAG CTGGTTGAGC TCTTGCTGCT TCCATATCCC TTTGTAGCTG 240

CTCTCCACTT TTCTGAACCC CGGGTCCATG TGAAAGTCCC CACAAGGNNC TTTGCAAGTA 300

GAGAAGNCG 309

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 904 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTTCATTTAA AACNCGGGGG NTGAACCCAA TCTTNANGGT GGCAGTGNGG NNGATCTTAA 60

CGGTTTTTNA GAAAAAAAAN TNCTTCGCTC NCACCCCCAA GCCTCCCNTT CTTANCAGCT 120

TTTTTATANG AAAAAAGATG ATAACGAAAT TTTAAAAACC GTCGTTAGAG GAAATGAAGG 180

TTCAGCCGAC CATTACCTGA NAGTAATGAA GGTNTTCCGG AGGGTTGCCT TCCAATCCCA 240

GATGGATTTG AGTTTCAGGA TCAATTCAGT TACCGNTGAC CATCCACCNN CCTCCNGTAT 300

AATCATTNGA TGAGGATGAA TGGTGAGTGA GTGATGATGA TGATGATGAT GATGAAGGGA 360

TGAGAAGNAC ACTATGATAA CAAGTGTCTC AGTCCACATT AAGGTTTGCC TGNAAATTAG 420

TGCATAAGCC ATGGGAGACA AATTCTTTTC NNACACAATT AATAGTNTCT TANTCCTTCC 480

CATCTTCTCT GCCCCATTCT GTTTTCCACC ACAGGTCTGC AGCGGGCTAC AGCTTCCAGT 540

CTCCAAGCAA ATACCAGAAC TGGAGGAGAA AATTCCAGTC CAGTGAGTCA TGGGCAGGGG 600

GAGGGGTGGG GTAAGGGCAG TGGCGCTCAT TCCTNACATG GTGTCTTCTC TTGCCTAGCC 660

TGGGATCTGA GGGCAAGAGA ACCTGTAAGC TTGATTTGAT TTCCACTGCT GACTGGAGTC 720

ACTGCCAAGG GATTTGGGAC TTCTCCATCT CTCTCTCTAA CCTGAAATCC TTAGGATTCT 780

ATTATTTCAC CGGACCAGAG CTGTAGCAGA GATGAGCTCC AAGTTTGAAA TGAGAAAGGG 840

GAAATTGAGA GCTATGAGCT AGGNGCGAAA GNCCCCACAA AGNNTTTGGC AAGTAGAAAA 900

GNCG 904

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 883 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGGGGGGGAA ACTTNTTTAT NTGGAAAANT TTTGTTTNGG CGGGNAAGGA GTTTTTAANA 60

ANGTTAANGG AAAAAGCTTT TANTTAANAT GACCTTTTTG GGGGAAANAC AAANTTGGTN 120

NGTGTATTNG NGAAAAAGAT TTATTATAAG ATTTTTTATA ANATTTTNGG GGGGGAAATA 180

TTTCAAANAA AATTCTGTAA CAAAAGGNTT TTTGTTTTTT GTTNTCCAAG NAGTTNTCCA 240

GGTAGTTNTC AACAACNNAN GCCNTAGGGA AGGACATCAT ATGGATATTT TCANAGATTT 300

GTTTTTAGGA AACATTNTAA AGTCAAGGTT AAGATGACAG TCAANTCCCA NGAGNGNGGT 360

AACTGTNTGC TTCTTTATTT AAAATTCAAT ATTCAGGATT TCATTTATAC TAACAAGANT 420

AATTACCATC TTAATGAAAC ATAATTTGAA TAATTTGCAA ACAATNTGAT TTTTCTTGAA 480

TATACATGTT ACTAAAATAT TANGGATGCA AATAGNTAAT AAACAAATAG ATANGNAACC 540

ATGGNACACC CCTTCTGTGA TTGGNGGGAC NTGGGCATAA GGCTTGTTTG TATAATAATG 600

TTCATATTTT ACATTCTTCC TNNGAGGANG GTCCTCCCTG TTAAGAAAAN GACTCCAGGA 660

TAAGGAGACA GCACCAGTNT AGGAAGTGAG GNTCTGTTTA ATGTCTTAGC AAAGTAGTAA 720

ATGNTGGGAC CATCAGAATA GCCCNTAAGG NTGTGGANAG AACTCTAAAA GCNTGATATA 780

TATATATATA TATATATATA TATATATATA TATATATATA TNTATATAAA GAGGCAGTAT 840

TGAAAGACNT NCACCAATNG AGCTGGCNAG CTAGAAGAGG TCG 883

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 924 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TTTGGAAGGN TTTTNAGGAA AGAAANTGTN TTTNAGGGNA GGGAACCCTA TTCCGACGGG 60

TTGGGGGAAA ATTTTGGGTT GACCCTTCGT TAAAAAGGGT TNCGGTAAAA GGGGGCNANG 120

TNTTNNAANA AAAATAATAG TAATAGTAGT AGTAATAGTA TTAATAATAA TAATAATTGC 180

AGGAATCCTG TNACCNTCAG GAATTGGGGA AGTAGTTTCT TATTTTAGGA CCAGGTGTTT 240

TGTTTCAGGG GAGTTATTTT TTGTTTTGTG GATGGGATGA GTGGTNTCAA TTGCTTTNAA 300

AAACCTGTAT TAGTTTTGGC ACAGTTAGTG TGTNTCNGNT TCGTTNGAGG AGTTTGAACT 360

GGATGGTAGG CAATGGNTGC ACAGATTCAT AGTGGCCAGA GTTAGAGTAA ATGCTTGCGG 420

AGCAGTCAGA ATAGATGAGA NTCAGGGACC CGGCAGATGA TGCAGGGAGA ATGTAAGAGC 480

AGAAGGTGGT GGGTAGCATG TGGAATGCAC ATTTCCAGGC GTGACATGAN TCGGAACAGC 540

TGTGACTGCT TAGACCAAAG TGATCCCATC AACACGGCCA TTCAGTAAGG AAGGGTCATG 600

GGNTCCCCCC NTCCCTTAGG ATTNACATAC AGATAATGAT TGATTGGTGG ACCAGGGGAA 660

TGGGGAAAAA TGTCNTTTTC GTTGGTATAG TCACTGGTAG CTGCCCATGT TTNTATAAAC 720

AAATTNTAAA GAAANTCATT GGTTCATACA CGTAAGAAGA CATCAAAACA GAACTGAGGC 780

AAGTTGGGAA GAGAAATGGG ATTAGTAGGA GAGGGTCAAG AAAAGGCAAA GGTATGTGCA 840

CATGCATGAA TACATTGTAT ACATGTATGA AAGNGCCACA ATGATGANTT ACCCCANATG 900

GNNGTTTGGC AAGTAAAAGA GTCG 924

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 482 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCTCTCCTGA GGGGGGTTTT NTGGANGAAT AGAAGAANAN ACCNCCTCTT TGTTTCNTCC 60

TGTGGNGNNC CCTGCTGNTA AAGNNGATTT NCNCGGTGNT ATACANNTAA GAAGGAGGAT 120

CTCTCCCCCC ATTGTNANAG AACCCCGTGT GTGGGGAGGG GGTGTNGCCA CNANCCAGAN 180

NTGGCCCNNG GGTCNTCTCC CCACTCNTNT GNATAACNTC TNNCCTCCAC AAANACCCCA 240

NANAAAANCA CCCCNCNTGT GAGNNCNGCA GANGCGCCCT NTNACAAGAN AAGAGNNCAT 300

GTGNTGTGGC CCTGTGCTNN GACANTNTAN ACTCTTCTNT NGNGGGGNGN GGNCTGTGGT 360

TTTATAAGAG NGTGTNNCCG TGGGGGGGAG AGTANTCNTT TTATATAGAG AGANAGNGNC 420

CTGTGNAAAC TNCCTCTGAG AAGAGCACCN TGGTGTTCTC TCCCATCTNC TAGNAGGGGA 480

GG 482

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 460 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TAGCTTCTCT GTGAGGGGTA GAACTCAAGC TCCCCCATGA ACAGGCTTTG GGGTTCCTGC 60

CATCCCCTGG GGCTGTTCAT TAGGTGCCCA CACAGACTTC TCATGCCATG ACTCACACTT 120

GACGTCACAG AGCACACAAA GAGCACAAAA GCAGGCTGAC CACATCCGGC CATGCACACC 180

CCTTTAACAG TCCCAAGCTT TCTCTCTCTC TTCTAAGTCA CTGCCCTGGG AAGACGGTTT 240

CATACCCAAG CTGATGTGCA CTTATTTCTT TGTGTTATTG CTCTGACAGT CTCACAGTGC 300

TCTGCAAACA CTCTGCATTC GCCTTTACCA CACCAGAAGA AATTCCTCTT TGTGCAGGGA 360

AAAATACATT CGTCTTAGTA GCTTCTACTT TCCAGCTTGT CCCTAGTCTG TCTGATATGT 420

GGTTACGTAN TGTTAGGGGC CACGGAAGGG GGGGGGGGGG 460

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TCCCAAGACA AGAGGGGCTG AAGAACGGGG GGGGGAAGAA TCAGGAGTGT GTCGCTGCTT 60

CCCACATAAA GACGGCACCT ANATCTGTCT CTCTCGGTGT CTCCTCCCCA CCTGGGGCAG 120

GGTGAGCTCT CTAGACAAGA GAGAGACTGT CACAGAGAGA GAGAGATGTG TCACCCCTGT 180

GGAGATCAGA GNCNCCGACA CCTAGGGGAC AAATGGGGAT CTCTTTTTTT TTTCTCTCTC 240

GAGACAGGGG GTCTCTGTGC AACACTTGCT GTTCTGGAGA TGTTCTGTAG ACCAGGGTGT 300

CCCCCAACTC AGAGAGCCTC CTCCTTTNCA CAACTGTGTC GCCGCCGCCG CCGCCGCCGC 360

CATCACCAGG CTATATTTAC TATTATCTCT ATTACTATTG TTGTGTGTTG TGTTGAGACA 420

GGATGCTCAC GCATAACCCT ANCTATCCTA GTGATAGACC CCACC 465

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 568 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TNNCNNTTNC CTGNGGCCGN GTANCTCTGA GNGANAGTNT CCCCGAGAGG GGGGGTCTCA 60

CNNTAGNTNT ANANAGTATN GNGTGCTCGA GTTTNNAGAG AGCTCTCTCT NNNTCTCTCT 120

CCCCNGAGCT ATNGNNTTAG GGNTATGGCA CNNCNCGTCT CTCNNCNCCN TATNGAGNGG 180

TGNGNTATNG GGGNGAGAGT NTCTGCCCGA GACCCACATT CTCNGAGTNN GGNAGAGTNT 240

GGGAGACACA CANCTCCGGG NANATCTNTC TCCNCCCCCC CAGGGGCGGT GGTNCANATN 300

GNCNACAGAG CCNCNGNNTT NTATGTGGAG AGGGGATATC NCANCNCACN CCCNGAGCAC 360

AGGNTCCACA CNCAGAGANG TGTCTCTCCC CANCACACAA GCACNTCTGG TGAGNTCTAN 420

GTTTTGNGAG AGACNNTGCC CTGTCTCCCT TTTCCCCGCT CTNACACACA TGAGAGGGTG 480

TGCACATCTT CCCCATGTCC CTCTCTAAAA CCNCCCCAGA NTTTTGNGGT TNTGTGCAAN 540

ACCCTTTTCA CNCTCANGGG AGATNTTT 568

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 920 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GAGGGTTANT TGGCCCAANT CGGCAATCAT CCNGGGAAGA AGANGNCAGG GTTTNGGCAA 60

ATCGGAAGAT CAAGGACGCA ATTCGNGGGG GGGGATGGAT AGNNGCNAAA GGGNACNGAA 120

AGNNGGATTG GNAGGNAAAA TTAAACGGGA GTTGTAATCC AAAAGGACGA CAAGGCAAAA 180

ACAAATCCGG NAGTAAGCAG GAAGCACAGT GAANTTGGGG GAGGCAGNGT GGNGNAANTA 240

AAAAATNGTT TTTTTAATCC CAATANGGTC AACANGTAGG CAANTGGATN TATTAGATAT 300

TATATCTTAG CGCAAGNTTN TCACCCATTG GTCCAACCCA TATAACATGG CGGTGGTNAA 360

TNTNTGAGCN TGGCACAATT TTTNACCCAT TAGTTCCCAA GGCAGATCGC CACCATGCCA 420

GAANAAAATC CCAATTCCAT GGTGGCCCAG TGTGTCCAGC CACCAATANT TTCTTGAATT 480

CAATTAAATC ACCACATGAA GGAATACATA ACACAATAAC ATCTGATCCA ATTGATAAGA 540

TATAATTTGC TCACNTAGAC ATACAAAATC CTGTACATTC CATCTCTTAA GAATATTCAT 600

AACAAACTAT AAATGTGTAG AGAGGAATTT TAATATCCAC TTCCATGTTC TCTTGGCTGC 660

TCCTCTCTCC CAGTCTCCTC CTCCTCCTTT AAAACTTTTT TCTCCCACCC ATCATTTTTT 720

TTTGTCCNAA GGACGGGCCT TGTTNTATCC TGNACCTGCN TTCGTCTGCA TAAGGCCATC 780

ATCCCACAGG CAGGACTGGA GCAATGGCTC ATTGGTTAAG AGCACTTGCT GATCTTGAAG 840

AAGACCAGGG TGCAATTCTC AGAGCACTNC ACTGCTNCAC ACTGAAAGAC CCCACNNGTA 900

GGTTTGGCAA GTAGAAGAGA 920

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 176 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTGACCATAT TATTTTTATT CACGTTGGGA CAAAAGAGCA AACGCAAAGG ATAGGAAACG 60

AAAGGAATTA ATTTCCTTTC AATAGAGATA TCGGTTTTTT TTAGAGGGAA AAAATTGAGT 120

ATTAGAAAAT AAAAATAGGT TTCGGAATTT CCGGAAAGAC CACTAAATTG TAGGTT 176

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 336 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AAAAGGGNTN CCGAANAAAA ANAATTNGGA TCTTNTGGGG GCCCNGAGGN AAAAAAAANA 60

NTAANCNGGG GGNGACCCAG NGAANAGACA AATTNTTTTN CCNGGAGTCC TTGGGGTGNN 120

ANGCCAAACN GNCGTTTANN GNAANNNGNC GNGNTACCNC TTCGGAGNGG GGGCGCTGNA 180

AAAGAATNGT GAGAATNCNG TTACNNGTGT TGNTTNATCN GAGATAGTNG TNTGTAACAA 240

CCCCGATTCA GCCNGAAAGT TACGCATATG CGNANCGTTG TGTGAATCGA ACCTGGNNAA 300

AACAGACCCA TNGNCAAGNG GCAGACCNAA CGGAAC 336

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TGAATAAGGG TACAAAGATT GTGTTTCAGA GGAGAGAGGT AACAAGAAAA GACTCCTAAC 60

GCAATGGCCA GAGGGCCAAG AAAAAGGGAA AA 92

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 838 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGNGTNATTT TCTTCTNGTG AANTCTTTNC CAAATCCGNG GGTNTGNCCC ANNGCCCCNN 60

TTTATACACN NNATTACNCN TNNNCCAAAA CNCTATATGT NTCGANATGT CCCATNTTAA 120

ANATATGNGA CTCAGTTTGA GTNTCCCCAN NTTGGNGTTG GGGTATNTGG GTAAANACAN 180

NGACCCTCTN NGGNGNTTTA TTTATATATN NGNCCCNATA TAACNCAGAG ATCTGTGTAA 240

AAAATATNNC NNTTCGCGGG GNGGGAGATT TCTCTCTGNN GTAGNGCNCT CNNCTGAGAN 300

GCACAGNGCC CTGTGTTNTN TCCCCCTCNC CGAAAANAAT TTTNTNCAAA AANANANAAT 360

ATNNACANAC CCCNANAAAT ATNCCCCTTN TCTACCNCCC CTCAAANACA CCNCNNTTTT 420

TTTTTNCCCC TCAGAAATNT TTNTAATNTG GGNNAAAAAA ATCTNNGNTG GNNTTNTCCC 480

CCCNTTTNNA GNCGCCCCCT NNAAACCCCC NCTNTTNANA GANAAATATG TANACTCNTA 540

TTTAAAAAAN AACANTTTTT GTTNGGGCTN GGGTNTNCCA NCCCTTCACT CTCTTTGTGG 600

GTNTNCCTTN CCATATNCCC CCTNTTTGAG ACNTTTAAAN AACCCTCTCC CTAATTCCTC 660

CNCCCNCTGT TTCCCCCTTT TNNAAAAACN TCNGGCCCCT TNGCCCCCCT TTTCTNACTC 720

CCTCTTNTCC NGAGATTTTT TCCTCNTNNT NNCTAATTCC NTTNTTCNAN TCTANATNNC 780

NNTGTTNCNA NCGCANGNTN NCCCCNCCTT NNNCTNAATT NTNGGGNAGG TTCCAACC 838

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CAAACCAGAA ATGGCCCAAG GGTCATCTCC CCACTCAGTA TGAATAACAT CTAACCTCCA 60

CAAAAACCCC AAAAAAAAAC ACCCCAGATG TGAGAACAGC AGAAGCGCCC TATAACAAGA 120

AAAGAGAACA TGTGATGTGG CCCTGTGCTA AGACAATATA AACTCTTCTA TAGAGGGGAG 180

AGGACTGTGG TTTTATAAGA GAGTGTAACC GTGGGGGGGA GAGTAATCAT TTTTATATAG 240

AGAGAAAGAG ACCTGTGAAA ACTACCTCTG AGAAGAGCAC CATGGTGTTC TCTCCCATCT 300

ACTAGAAGGG GAGG 314

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 226 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AGGGGGGGAA ACCCCTTCGC CNCGGGCCTA TCGNAANTTT TNNTCCACCG TAAAANATTT 60

NCCANGNGCN CCATGTANGG ATTGNGGGNG TAGTGGGGGG AACGATTNTG GAGGGGCCTA 120

AAAGGNANAT AGAGGACGTA TTGTATTTGG TTTTGCNGAG CCAGTACCTT NGAAAAAGGT 180

TGGTATTTTT GATCCGGCAA CAACCACNGT GGTAGNGTGT TTTTTT 226

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 843 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GAATTAAAAC GGGAAAGATT GGAATTCAAT TTCTTACAGC CAAAAGCTAG ACCGGGCATA 60

TAGGAGATTA TTTCGATTTA GCACCTTCCA AAGCCTGCCC CAGATTTAAA GTTTAGGGGT 120

ATTATTTAAA AGCAGGTTCC GGGAAGTTCC AAGATAGGCC TAGAGGTAAT GGTATGCAAG 180

CAGTCCTAGG TTTCAGAAGA GTTCAAACAC GGGTCTTCAG GAAAAGACGG AAAGTGTAGA 240

TTGATCAGGC CAGCAATCAT ACAACAGTGT TTGTTGTAGT ATTACCTTTT CTAATGGTTG 300

TCACTGAAAG GAGATTATTC TAGGTTTGGA GATACAAAAT TAAAAGAATA AACCCCAAAA 360

GGCCACAGAC CCAGGGTAAG CCCTGTAGCC AGGACTAGCA GGCCATAAAG AAAAAGGAGC 420

ACAGGAAACA CTGTCCAGGC AGGACTGGCA AGCCATAAAG ATAAGGAAAA GGAATGCAGG 480

AACCAGCCTG AGTTAATGAG AAAAATTAAT GGGACGTCTG GCAGGAAGAC ATCTCCCCCT 540

AGCACACTCC GGGCCATATC TCAACTAGGT GTCCTCCAGC CCCTGACTTA TAGCACGTAC 600

TCTATCTGCT TTGTTATCAC AGATATGTTT GAATGAGCCA ATTGTATGTA ACCACGCCAA 660

AACCCCCTAG CTTTGTCTAT ATAACCGTCT GACTTTTGAG TTTCGTGTTC AACTCCTCTG 720

TATCTTGGGT GAGACACGTG TTGGCCCGGA GCTTCGTTAT TATTAAACGA CCTCTTGCTA 780

TTACATCATG ACCAGTCTGG TCCTGTTGTA AGACATTGGC AAAAGAGCCT GAAAACTAGA 840

AAA 843

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 943 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TTTTTTTTTT GGAAAAACGG GTTTAATAAG GGGNANGNAT CCGAACCCCC ACTCGGGNGA 60

AAGGAAANAA AANAATANGG GGGGAANAAN GANTTGGNGG TAATGCTTTA CCACGACAAA 120

CTAGTCCCAT TNTTCGGGGG GGGAAAGGGA NGGCATGAAT AATGGGGTGA AGGCNGGCAC 180

CCACCCCATT TTTTCGGGGG TAAGTCNGTT TTTTTTTGGT ANATCAAAGT TCCTTTCGGA 240

ANATGTCCGT TTNATCCAAG GNGTTTTGGG TGTTNNAATT AGNATTTNNG NGAGTTTCAA 300

AAGTTTGTGT TCNNGAGNAG TTTGTAATTG GTTCAGCNGG TTTTTTTGTG NCAGGAAAGC 360

AGACCCNTGT TTGGGAGGGA GATCCAATTT TNTAGTTCCC ATTTGGCTGT TTCCTTAGTA 420

ATGGGTCTGC AGACAGTNTG AAGTNTATGA GTTGGTCCCT TCTCNTATCA GCCCGGGGTG 480

GCATTNTGTC CAAAGGAGGA AATCCAGCAG CCAGACTAGA TTTCAGTNTC CTTTNTAACA 540

GGGAAGTTAG ACACACCCGG CCAGTTGCAG CCTTTCCACC CCCAANGAGT GAACCCTGCC 600

NTTTCAGNTT TNACCCAATT TACTTTCGTT GGCTTAGCAT GCAGANTCTT TGGCTCCATG 660

CCCGGAGCAG CTGACATGGG AGGCTTTGAA ACTTCCATTA TCATAGAATG GCAGGCAGGT 720

CNTTTGCGGT TAAAACCAGG AGCNTGGGCC AATGAGATGG NTCANTGAGC AAAGGCGCTT 780

ACTGCCAACC CTGATGCCNT CAGTTTAGTN TTGGAATTCA CAGGGTAGAA GTTGAAAACC 840

TTTGACTCTT CAAAAGTTGT CCTGTAGCAG GGCAGTGGTG GTGCANACNT TTAATTGNNG 900

TACTTGTGAT AGTCCCACAA GGANCTTNGC AAGTAAGAAG TCG 943

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 904 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ACTTCTCTAC TTGCCATGGT CCTTGTGGAA TCTTTCAATC TGTGTCCTTA GAACGCTAAG 60

CTAAGACTTG ACCTTGGCTC CCAGGGCGGG CTGGGACTTG GCCACCCCGT GAAAAGGGCT 120

CTTTCTCAGG CAGGTGTTTT CGTTTAAGAA AATAAACCAT CCAAGTCCGG GCAGACTGAG 180

AGCTACACAC CCCTCCAAGC CAATCTGGAG TGGCTCTGCC CAACCCCCAC TGCTGGGAAA 240

ACATGGCTGC CTCAGCACCT CCCTAAATGA AGGGAACAGA GTGTCTCCTG TGGCCTTGAA 300

AATATTAATA AATGAGACTT AACCTGATGG CTCAAGGCTC TCAGGGGGCT TTTTTTTGTT 360

TTTACACACT CTGTGGAGCT GTTACAAGGT CAGTCAGTCA TTTGCATGGG ACAGACAATC 420

TGTTTTAATA TTTTATATGT TTGTCTTTTA AAAAACCTAA GATCTATATC TTTTTACATT 480

TTATTGTTTT GTTCAAAAAA AAAAGTTTTA CACAATGATC AAAAAGTTCA AATGAAGTCT 540

TTTTTAAACC TCTCTCCTGC CAAAGGAAAC CAAGCAAACT TTTTCCAGAA ACCTGATAAG 600

AATATCTCCC TTTTACCCTG GAAACATTAA AAATAAGGAT CCCTGAATTA AAAATTCTAT 660

TCCAGAATCC TAATTTTATT TTTTATTAAA AAAAAATAAA ACCCCCTTAA CTGACGGGCG 720

GTTTTTAAAT CACCTGCCTT CAAAACCCCC CTGGAAATTT TTAAAATTTT TTTTTTGTTC 780

CCCAACATTC CTCCCCCCCT AATAACACCT GATTGATACC CACCAATTTT CCACTGTGGG 840

TGATTGAGGT GGTCCCCCCT CTTTTTTGCC GTTTGATTTC CCCCGTTAAA AAATTTAGAA 900

AAAG 904

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 917 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

AAGGGGGGNG AAATTTAGNG GACNAAAATT ATTCCTTAAG GGCCNCCTTT CTTCAGGGAA 60

NANGGGGGAA GGAGATANTN CGGCCCTTGT CCGCCTTTTN GGANACGATA GGGNCGGTTC 120

GGNTTGGAAA TTTTTCCTCC AAAATTNCCA ACAAAAATNG TTTTTCCCCT TCCTTCAAAA 180

AGAAAATTGG TTTTTTTGNN GGCTTNGGGG NGTCNGGAAG TCANAACCCN GNGTATTATT 240

GCNTTCCAGC CCCACCCGTN AGTTCATTGG TAATTCCTAT TCGTTCGGNT CAANATAATT 300

CGGNACTTCC GCTTCCNAAT GGATCCCTTC AANGATTNGG TTTTTCCGGA TTATCGCAAG 360

TCCCCNGGTT NTCCAATCCG GAGCGCNTCG GATATTTCCG GNTNTCCGTG CNTTTCTAGC 420

CCCACCCCCA NGACCACCNT TGGTTNTTTA GGTGGGTCTT TGATCCGCTT CACGTTGCTT 480

CAGTGACNTA GATCCTTNTT CGGTCTTTCC GGCTCATTTT AGTCTCGAGT TATTCTCAGC 540

TGTGTTANAA AAAAACANNA NAANAANCTC CGCCTCGCCC TTCCGNTTCG GTTCTTTCCG 600

CNNGCNTTCG GGCGGGCNGT NTCTGCCTTC TCCACGTGAC GNTTNTTCGG CNTCCCAGTN 660

ACCCCCTCCN TCCACGCCTT CNTCCAGNTT CAGCTTNTGT GCTCGTCCCG GNTGTGCCGC 720

CANNTNGTGT CAATTCCNGA CCGCGGCGGG GGCCGGGCAG NTGGGGNATN TAGGGCGGGC 780

AGACAGTCGG CCNATCTCCA TAGGCCGTTC CCTATNCTNC CCTGATTTTT TTAAACCATT 840

TCCAAAAGCT CGCTGTCCTC TTTCCGGGNC TTCCATTNNG GNGTNTCCAN AAGGAAGNAA 900

GNCNAGTAAA GGANCTC 917

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 835 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GGNCCCCTAN NGATTGGCCN TTGATCAAGA NGGGACCATC CTGNACCTGG NGGTNGNTGT 60

TTCCGCTTGG GACGGAGATG GTTGTTTTTG CGGAGTAGTT TCNGNGGGTT TGAGGCGCGG 120

NTANTTTTTT TGTTNTGGTC CAGACCGTTT TGATTTAGCC GCNGCNGACA GTAATGGGGC 180

GATACCTCAG NTCCTTGTGA ACCCAGGGTG CAGNTGGTTC AGCAGGATAG ATGTACAGCC 240

TCCGAACTTT TCAATTCCCN GACTAACCAT TGATGTCAAG TTGAGTGTTT AAATGCTTGC 300

TACCAAGCTG GTTGGTAACC TGAGTTCAGT CCCTGGAACC CACATGGGGA GAGAGAACAT 360

GCTTCTGTAA CTTGTCCCCT AACTACCCCC AATACACGCA TGCGCGCGCG CGCGCACACA 420

CACACACACA CACACACACA CACACAGAGA GAGAGAGAGA GAGAGAGAGA GAGAGAAGCA 480

CAAACAATAA AAGAAAAAAA TAAAATCTCA TTTAATTTTC ATTAGTATAA TACCTTGATT 540

CTTTGAATGA CAGCAAGATA AAGTAAACCA AAGCACACTG TAGAAGGGAT TACGCAACTG 600

AAAAGTGACA ATCCTTACTC CAGCCCTTCC TGCTATGTTG GCAGTCTTGC TGGGAGCCAT 660

TGATCTAATC AGTTTTATTT GAGGCAGGGG CTCATGTAGC CCAGGAGGAT GGTCAAATCC 720

ATAGCTCATC TGAGGATGAG TTTGAACCTC TGACCCTCCT CATTCTCCAG TTCTCCATAT 780

CCTGAGTGCT GGCACTGAAA GACNCCACNA GTAGCCTTGG CAGGCTAGAA ANGNT 835

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 924 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GTNTTTTNGC CGNGGGAATT TAAGGGNGAT TTGGAGACTT TNGAATTTTC GAANGTTCCA 60

AAATAGANNT TNAGGNCAAT GGGNTTGGGG CAGNGGNGCT TTTTTAAATC ANANAAGTAT 120

TAGATTTNTA TGGAAACCCT GGGGGTTCCA GTTTAATCCC TTCATCATCT TGAAATATNA 180

CTTGTTTATG GGAANGGTGN GATAGCAGCC NGAAACAGAG GTTTTTATTA TTACTGTTAG 240

AGANGAGGAT TGGGGAATAG AACAATGAGA GTCTTGGTAA TATTNTTCNG GAAACAACNG 300

ACATAATTGG AACATTAAGG AAATATATCC ATGCATTCTG TACTTGCAAA TTGCTCCAAG 360

GAAGATGGAG AGTATTGTAT TTCAGATAGA GATANGACTA TACCTGTTAT TTTTTTCATT 420

ATAGCAACAT TAAAAAAGAT AGTAATCTAA TTTCACATAA CCATTACTAC TAAAGTATAT 480

ATGTANTCTT TGTTTATCAG GTTTTACTTC TCAGAAATTG CAGCATCTCC TACAGAGCCT 540

GTCAAATGAG ACNGCATAGA TCCCCAGAGA ACAGAGAGAC TGGGAAATCA TTGAAATTAC 600

ACAATCCTAT CCCAAATGTT TGCGTAGACT CAAGCTCGTA TCAGCTCATA AGATCAGTGT 660

GTGTGTGTGT TTGTGTGTGT GTGTGTCCCG CACATGCTTG AGTATGCATG TGTGCATGCA 720

TGTGTGTATG TCTATTGCAT TAGTAGAGAT GTTAAGGTTG AATGTATTTT CTGCTCATGG 780

TCATTGTAAG ATATTGTGCT GTATGTGATA AGAATCAATG TAACAAGGCT GGAGAGATGA 840

CTTCAGCTGT TAAAGGCTAG ACTCACTACC AAAAATAGNG CNATCAGTGT GAANTTCCCC 900

ACAGGAGCTT AGCAAGNTAA TAGG 924

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 435 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GATTCCAGAG AGAGGAGTGA ACTGGCAGAT AAGGCAGTCA GCATAATGGC TTAGATACCA 60

TGTGCTTTCG CTCACTATGC ACCCATGACA CAAGATCACA GGGTACAGGC CTGGACCATG 120

GCAGAGTATA CACTGGTTGG GTAAATGAAG AGGAGAGACA GAGTGGGAAG TCGGCTTAGT 180

GGATATGGAC TTCAAATTTG ATGAACAAGC AATTCAAATG AGTATCGTGG GCTTGANTGG 240

TATGAAGACC CGTTTGCAAA GCAGTGGTCA TAAGAGAGAA AAGAGAGAGA GAGAGAGAGA 300

GAGAGAGAGA GAGAGAGNAA GAGAGAGAGN GTGTGTTGTT GTTGTTGTTG TTGTTGTTTA 360

TTGGTTNATA ACAANATNTA CCTTTGGGCN CTTTNGAAAG ACTNTNCACA AAGGAGCTTG 420

NCAAGCTAGA AAGGT 435

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 919 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CCCCNGTTAC CCNGANGTTT ACNNGTTGGA TTAAANGGGN NNNAAAACGG GTGGGGNNAA 60

ACGAATTTTT TGTNCNCGAC CCNTCCCCGG TTGGGGNTGG NGAAATAAGT TTTAAGGTGG 120

GAAANGGAAA GGAAATAAAA ANATTTTTTT TNAAGGAAGT TCCTTNCCAC AAAAAANTNG 180

NTTNGTTCAG TAGGGTTCGG GCCCGGGAGG NAAGGCAANN TTGAANTNCA NTTAAAAATT 240

NCCNGGAANG TACCTTGGGN AGGGATTACC NTGNAATTTN TTTAAGAAAA NNTGGGTNTT 300

TTGGGGNGAT TTTNNGCCCC ACCTGGACCA NTTTNGGGAA ANGCAGAAAC GTTCCAGNGN 360

GTTTTCCTTC CAGAGAGAGG GTTAGGTTCC TTCAGGGGNT TCCAAGGACG GGGACCAGAA 420

NGTGAAACAA ACCAGGNTNT GAAGAGACCA GNCGGGGGGG GGGGAGGGGG CCGTTNTAGA 480

TAGATTGAAC CTGCAGAGTT GCCTGTTACC TGAAGTTGTC ACCNTTTNAC CNACANACTT 540

NATAAANNTN TGNTGACCAT NTCAGCAAGT GTCACCTTCG TTGCCAGGAC ACAAGTTTCT 600

TAAAGCTTAT TTCAGTNTCA CCCGCTGGGG AGANACATTC AGGGCATGGG CGTCCCCCAG 660

CCNTCGGGGA GAATGTGGGA GGTGGCGATG TGGGAGGGAT TCGAGAGAAG AGAATGCTTA 720

AGAACCATCC AGGGAACCTG TGCGTTTGAA GGTNTGAGTT ACACACAGGC TGCTCAGGAA 780

GGAGCTAGAG CTCCAAATAG GAGCTGTGAT CAGGCTGTGT GTGTGTGCTG GAAGGGCCAG 840

TTAGCAGAGG TTGTNTTGAC CACCCAGNCT ATTGAATTGN GNNTNNTCCC AAANGGANNT 900

TTGGCAAGTT AATGAAGTC 919

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 915 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TTTTTTGGAA TNTTGGAACC NCGNTTTGGA AGAAGACCTT TNNNNTNCAA TTGGGGAANA 60

ATAACCGGGG CCAAACCTTG GGAAGGGGGG AAAANATTCC NGGGGGGAGG TAATTTNTTG 120

GNNGGNAGGG GNGGAGGTTA NTATNNCGGT TGNGGAAGTT TGGAATTGTC CNAANGGATT 180

TTGTTTAAAA AGAGGNTTGC NGGGCNTGNT CCCTTCAACC ANGAGGTGGG GCCNTTGCAT 240

TTATTTTCCT TTTAACNTTT GAAGGTGAAG CCGGGTTATT TNTTTGTCCT TCGTACATTT 300

ATCACCACGG NGTTTAAAAN GTNTTTTTAT TTCGNTTTNA TGGAGGNGAG TTAAATNTCN 360

ATTTCCAATT AAACCTCNGT GAAACCTTCT TTGATCCTGC CTNGTGTTTC CTGAGTGNGA 420

CATACCTGCN TAGTTNTGGC CTTCCCTTTC CTTNTCGTCC TTCTTCCATT CCCTTCCGAA 480

GATTCCTGAA GGAGTGAAGG TTTGGGAAAG GGGGAGGGAC AGAGTGTCCA GGGCTTGCGT 540

GTCAGTAGAC ANNAAANAGC CGNAGGGCAG CCCGGGGTGA AACCACAAGG CAGAGGCCCC 600

AGGGTAGACA GCTGACAGGC CCGCCCACTT TGGCTCCTGC NTTCGCTGTC TCACCCCAGA 660

ATTTTCCTGG CAGGAGTGGA AGAAGTTGGT ATCGAGTCTT TGAGCCCTGA CTCATTNTCT 720

GTCCTAGCTG GGTGCTCCTC AGTTACATCT CCAAGTGTCT CTCAGGGGTT CAGTGTTAGC 780

CACATGGCTG CCTCAGNTCA AACCGGAAAC CCAAGAGGCG GAAACATGCT TCATTTAATT 840

CCCATCTGGG GACCCNTACA AATTTANGGN TTGTACTNAN GGATTNCCAC AANGNNAAAG 900

GCNAGNTAGA NAGGT 915

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 849 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GTTAAANANG AAAAAGNGGG GGTGACAGGG GGNGANACCC NTTGCGCCGG GCTATGGATT 60

NTNGGCACCG ANAAGATTTN CAGGNGACAN GGAAGGTGGN NGGGGANGGG GGAAAGTTTN 120

GAGGGGCCAA AAGGANAAGG AGGANGATTG ATTGGTTNGG GAGCAGTACT TGGAAAGAGT 180

GTGTTNGATC GGNAAACAAC CACGNGNAGN GNGTTTTTGT TGCAGCAGAG ANAAGNGAGA 240

AAAAGATNTC AGGAGATCTT GATTTTTTTC GGGTCGAGCT ANGTTGGGGG ATGNGAGGGN 300

ACAATTCACA AGATTTGTTC ACAGGGAGNT CNAGGAGGTG GTCCCANTAG CCGGTAGGGG 360

GGTTTTCTCA ANAAATGGGN TCAGTCAGGT GNTTGCCTAG ATCTTTCATT AGTTCCTCCC 420

TTCAAAGGGA NTTTGAAGGA GTGCTTTGTC CTGTGGAGCA ATTGACTCAA TCAATAAACN 480

TAAGTAATCT CCCGGANTAC TGNNGANGCG TTCCCAGAGA GGTCCCCCGT AGTNACCAGT 540

GAATCACAAT TTCCTAACCA TANGANTNTT GTTAATCTCA CCACATAAAC CCACAATTCT 600

CGCGTCCTTN GTGATGGTTT CAAAGTCNGG AATATNTTTT CCTCCATCCC TCCTTTCCTT 660

CCTCCTTNTA TCCCTCCCTT CCTTTTTTCC TTTCACAGGA TCTCANNATG CAGCCCAGTC 720

AGGCCTTAAA CTTGTGATCC TCCTGTCTCA GCCTCCTAGG TGTTAAGATG ACCCAAATGT 780

AAACCATGTC CAGNNACTTC CTCCTAATCC CATCTTCAGA TATCCTTTAA GACCAAATTA 840

AATATTAAC 849

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 925 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AAAAAAANAA ATNTTGGNGG ACCNAANACC ACCAATGGGT TTTGGGGTCC GANCGNNCAA 60

ACNTGNTTTC ANTGTTNTTC TGGNTTTNTT TGNNTAAACT TGGGGTTTTA AGGGTTNAAG 120

GTTCCAAACC CNATGTTTTC GCNCAATTTA GGCGGGGNGG GGAATCCNTT TGGGGANGTT 180

TNAGTATCTA GTTAAGAGGG GCCATTTNGA GATTGACACC TGAGTTAAAC TTCNGAACNN 240

AGNTGTNTAA TNAACCCGTG AAGGGGCTGA GGGGNGTTGG TTANGATNCT CAATNNTAGG 300

GNAAAAANNA ATGTGGTANG GAGACAGTAG NNTANTCGGA NCAANTNCGC ATCGGCCNTT 360

NNATTAATAA GCAGNCAATT GAGGAGGTTA TCCACGACAG NGANAGGTGC AGACCCCACG 420

CACACTGTGA CAGTGGTTTA TGTNACANNA TNTCGGGAGN GATGGNGCCA CACCNACTGA 480

GTTCCGTTTT GTTCGGNTGA AGGTAGGNCA ANACTGGCAN AGGTGTTNGG GGGCNAGACG 540

NGAGATGNGG NTTGAGCNTT CAGACCNAGN TNCANGGNNN NGGACNANGG TCCCCNGNGC 600

CNTTCTAGCC TNGAGCAGNT TCNAGAGAAN TATTCGNCGG GTATAGGTCG CCCCNANGAC 660

GCNAAACGAC CGNGAGCGAG GGCGGAACAG CCAATCAGTT CGANTTATCG TGTNTGTTNG 720

CGGGGTTTGA TCCCNGAGTT AGNTCAATGA GCCCANAACC CTGAGTGGAG GNACCGTCAT 780

GGGAGGAGAG GNGAGTCACC NGGTACCTGG CATACNGATG GACCATCCAG TANTTGGATN 840

GGAGGGCGAT ATNGTNANTC TTAGGGGNTC TCCTGAGGAG GGNATACCCG TGAGTTCCGT 900

AAGGGCGTTN GCAAGTAANA AGTCG 925

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 827 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GCCAGTTGCC CTCAGATGNC CNATACCCCA CNGGGGGNGT CTCNCCCCTC TCTCAANTGT 60

ACACACACTT CCCCATAGAC ACNGGGGACC ATAGCTCTAG GGGGAAAACA AAATNTTATN 120

TGTGTGTGCA CNTGTGNGTG TGTGTGNTGC CCCAAACACA GGGGTNTCTC TTCCCCAGNG 180

GCCCTAAAAT GTTNTNTGTT CNCCACTNGG NCCTCATNTN NACATACCCC CCNNGNCTCN 240

GNCCCNNATA CCCNGACANN GAATGTGTGN NTNCCCATNN GCGCTNTCAC CACCACAGNT 300

TTTNTAANAC ATCTCTCCCC NNNATATCTN TTNTTTNNTN NGGGTCTCAA TGGAGACNAC 360

ATATACACNA GTGTGTNAGA CACACCCCCA CACCCCAAAT GNGCGGGGGG AGGGCTCTTA 420

GCGCAANGAG AGNGCAGNGT GCTTACTCCT CGCCCCCTCT AGAAAACTCA CACTNTTNAG 480

ATCTCGGGAC TCNNCCTCAG CNCATTCTCT ATCTCCCANA AANACACAGA GNNACCCTNT 540

TTGNGAAAAC TCANNTGTGT ATAGTGCTCT GNGTGTNACC CCNAGNCCAC ACCCCCATAA 600

NANATNTNTC TCTCAAAACA TGTGCATGNG CGTGTAACAC TCNCCATCTC TCGGGCNNGC 660

TCTCCCCNTN ACATCTCTCG NGNNAANANA AATATATCCC CTCNNTTANC CCCCGTGTCC 720

NGGANAATAT TNCCCCCCTG NGACCANTCC CTCCCCGGAG ACCNANCCCC CCCGTGGANA 78

CCCCCCCCNG GNATCAACCC CCCCGGGTAN ACAACCCCCG GAACCCC 827

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 899 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AAAAATTGTA AGGAGTTGGG GGNATCCCCC ATAATTNAAA NAGGGAACAA NCCNTAAAGG 60

GAGGGNNGGG AANGGCCAAN ATTGGNTTAA AAANAGTANG TTTGGTTGAT CCANACACAA 120

GGAATTTGTT ANAATTTTNN TAATGGAAAT NGGGCACTTC AATTGGGANG ATAAAACCCC 180

AGGAAGTGAT ACCNGGGTTA TCAAGTNAAA CNTGATTCTT GGNGNNGAGG GAAAGGATAT 240

TGAATTTGAG TGAGTGCAGG TGAAGTGAGA CTTGGGAGNA CAGGTCATGC CCACCCAAGG 300

GAGGAGCAAG GGNTGGGCAG TGTAGGTGGT GNGGTGGTCC TTCCTGGGGT GGGCGGGGAG 360

ACAGATGAGA ACGTTATTGG AGGACAGGCA CAAGTGTTAC TGAAATGCAA ATCCCTGTAG 420

ATNTGGAAAA GTTCTGGNTT CAGGCTTGAT GCTTGGGCCG GCAACTGTGN ACTTTCCCTG 480

TACGTTCAGC CCCCCCACCC TTACGGAAGT TNTCGTCACT GAGANTAGTG GCTAATCAGA 540

GTCTTCAATG GACCTGCCAA TCAGAAAGGA AGGCGGGCTT TTCCGGGTGC NTAGGTGTAG 600

GATTCGCTCA GTAGTTAAGC AGTCTTAACT GGTTNTGGCT GCTGTGCTCT CTGTCCTGCC 660

GTTGGATTNT NTGAGGCATG TTCAGGCAAG CTCCAAAGTT GCGACATGGT GAGCACAGGG 720

GCAGGGGGGG CGGGCGGACG GGCAGGGGAC TGAGCAGTGG GAGCTGGTGT GGTGGGTCTT 780

TCCCGGGGCT GAGTTGGAAT CCGCGGCTAC CCGTGAGGTC TTAGCCACTC ACTAGACCCA 840

GCGGCAGTTT CTGAATAACT TTCCTTGTAG GGGCTGCAAC TCTTGAAAGA CCCCACCAG 899

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 852 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AAAACATTGG CNAGACTTGT AATAATTNCC NGTTNGGGGA AAANAGNGGN NTGNGCTTCG 60

GGGGNGGGGA NCCGAGGTTC CCCCCAAATT TCTTANNAAT TGAGGGANAT TNANGGGGGG 120

AACCGANNGN TCNNNAAGGN GGGGTTTTTC CCNTTNGCCC CCTTGGGGNT TNACAANTTG 180

ACCNTNAGTT AACGGGGANA ACCCGCCNTG TCCTNNGGGA GGGGGGTTCC CTNGGGAGTT 240

NCGTNGTGGG TTTCAGTTCG GACCAGGTCG TTNACTCGAA AACNGGTCCG CNGTATNCAC 300

CCGGTNGGCN GNCTGTTGAN NGCTAACGNG GTAAGTATTT TCATGTGTCC GAACGTGTTA 360

GACTCCAAGT ATGGCCATGT GCANGAACCN CCGGTTAGCN AGACGCAGAG CGTGATCNGN 420

GGAGGNTCTN CAGGNGTCCA ACCNGGNANG NCAAGATNCG TCGACACTGG CAGNACCCAN 480

TGGNGACTGG NNGATCAGAG GGAGNCAGGT ACGCNGGGAA ACAGAGTTGN TGNATTGGAT 540

CCGGNANACG GACANNCNAG NGGGNCNGTN GTTTGGTATG TGNGCTAGNA GGANGCCAGG 600

NACAGTCGGA AAGGNTGTCG GGAGGNTCNG ATCATGTCNT ACATAACCNC TCGTGAGTAT 660

GCGGTGGNTG TGGAGTTGNG CAGGCGGCAG NTAACGCACC AGAGAATTCN GATNTNTCCG 720

CAGATCGACA GATNTGTTAG GTGGGTCTCT GACGTTNAGG NCGANAGGAN NNGGGAGNGG 780

ATAACANTNT CACACAGAAT TTCACTGAGG CTGAAAGACC CCANTTGTAA NTGNCCAAGC 840

TAGCTGAAAT CG 852

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 967 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

AAANCCTTCC CGGNGGGGTT AAAANAGATT ANGGGTTTTC CGNGGGGAAN CCCCNNCCNC 60

CGCCTTCGTA ATTTGTCCCC AAGAAAAATT CCCGCGCCCN CAAAAANNAG GGGANTNGGG 120

GAAATNTTAG NGGCCANAAG NAAAAAAGAN AATTGTTTNG TTTTGGAGNC CACNNCGNAA 180

NAGGGGGTNT TAAACGCAAN AACACCGGGG GGGGGNTTTT TNTTNCAACG CGAAAAANGC 240

GGAAAAAGAT TTCAGGANAC NTGAATTTTT TNGGGTCGAA GTTCAGTGGG GGGATTGGGG 300

NGNNAAAATT TNANACNGAT TATTGGTCCN ACCTTTCTCC TTCCCNTCCC TNCCAAAATT 360

TTNTCCAATT TTCTTCTTTN TNTCCATTTC CCCACCAGGA GGGAGTCACC CACCTTNTGC 420

NGCAACATTC TCAGGGTTCT TCATTCTCAG TGTAACAGCA GNTCTTCNGG TTCTNGGGNA 480

NTCAGAAACT GGGCTGAATC ATGTCCAGAG TTGCNGAGTT CCCACATAAC AGATAGTGTT 540

NGNGAGATTC TCAGTCTAGA ACCATGTGAG CCAATCCCCA TCAAATCTCT TCTCTCANGN 600

ATAAATNNAA ACATNCTTAN GGGAGGCTCT ATTTCTATGG AGAAACCAGN ACCCATATTT 660

NGGGCTGGAT CACTCTTTAT TTCCATTATG GGATGTTTAA CAGTAATCCT GGTCTGCATT 720

CCNTAGGTGC CAGTAGCCAT CTCCTAGTTG TGACAATCAT CATTTTCTGG GGATGAGGGT 780

GGAGAAGGGG GCAGATATCA AAACTATCCT GNATCTAAGA AATGTTAGTT GAAATGAAGT 840

TGTCATGGGT CATAAAGTCT AGGATAAAGA GTGATGAGAT GTCACTAACC CAACTCTTTT 900

GGCCAGAACT CAATGAGGTN GTCCCATTTG ANTTACCCCA AAGGNGCNTT AGCAAGTAAA 960

AGGGNCG 967

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 700 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GGNGTGCTGG GATTATAGAT GCACTCCCCC AAATCCAGCT TTTTACCTGA TACCGGAGGA 60

AGGAACGGAA GTCCNCCGGC TTGCACCGGA AGCAGTTTCA CCCACTGAGC CATCTCCCTG 120

GTCTGTCTGT CTCAGCTTCC TGAGCTGGTG TTATGGCTGT GCACCACCAT AGCTGGCTTC 180

TTTATTATTT ATGTATGACT NGGGTCTNTC TGGGGGTCTG TTAGNCAGTC TGTTAACTAC 240

CATCTTTTGN CTCAGGCAGC TGCAACAGAA AACAACNGGC TGTAAATNGT TTTGACAAAT 300

GGGTCTGGGG AGAAGTCTGT NATGCAGGGA GATCTNGAGT TTATNCAGAG GAAAAGGTGT 360

CTNTCAGNGN ATCTAGGGNA GCATNTCCTN TCNGCGTCTT GGTTTGGGNG AANGANGGAT 420

CAAGAGCCCC NNAGCNNNNN AANTTNCCNT CGAGCAGCCC AGGGATTTTN GCTTTCAACG 480

NANCTNNAGG GAACCCCCNA NCAACCTNGG CNACAATTGG GGNNTTTCCC CCNCCCCCCC 540

CGATTACTTT TNCAAACCNT TGCCACNCCC TCGCNCNATG CCNANCCCCC AAAACGTCGT 600

NNTTCATAAN CNCNNCNCTC NCNCTTNNCC CATGGGGNGC ACACTCCCTT CNCCCNCNTN 660

TNTTAACNGG NGGCGCAAGN CCTTTCTTNC CCCCTNCCCC 700

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

NCNACGAGAN GTCAANGTGN AANCTGNCGA TGATNAAAAN AACCGANCTT AGGGTGNCAA 60

NGGGTTACCC AGGANGGGGN CAAAGCAAGN TCCAGGCCCA TNANGGACCT GCTGGTNCAT 120

NGCCNGNAAA NACCTACTTA TCCTNGAANA GCCCGAAANG TCCGCTNNGA CCANNTAAGT 180

NCANNNCAAN ANGNACCACN CCNTTAACAC CACCGTATGA NCCCNAANT 229

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CCCCTTTCGN NGGCCTCAAT NANTNATTGN CTACCCNANA GTGGCGGTCT NNCATCATGA 60

CAAATAAANC AGCCTTCATG AAATACGATG GCGGGGGGAT TAGAGGNNTT TNTTGAAAGA 120

GCTGAAGGGG CTTGCAACCC CATAAGAACA ACAATGCCAA CCACCCAGAG CTTCNAGGGC 180

ATTAAAACAC TACTGAAAGA CTATACATGG ACTGACCCTG GNCTCCAACT GCATATGTAG 240

CAGAGCAAGA GCCTNGTTGG NGCACCAGTG GAAGGGGAAG CCCTTGNTCC TGCCAAGGTT 300

GGNCTCCCAG NCCAGGGGTA ATNTNGGGGG CGGNGGAGCA GTAAGGGAGG GTGGATGGCG 360

GGGCTACCCA TATNGNGTGG CGGAGGAGAT CGNNGCTNAT GGACAGGAAA CTGGNAAACG 420

GGAATNACAT TGGANATCTC NATAAAGNNN NCATTTCTTA TTCNA 465

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 564 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TTGGGGCCGN TNAACTCTGN GTNNNAGTAT NCCCNANAGG GGGGGTCTCA CANCGGGTCN 60

CACCNCATNT GNGGGNGCCC NTTCNCNACA ACACATTTTG TCNGGNGGTT ATAGNGAGAG 120

CACANATTTT GAGAGTCNCC NGANAGGGGA GAGAGACNCA CACNAGTCTC TTCTCCCCGT 180

GTTCGCGAGN GNACNCTTCT CTNCACATCT ANAGTATANC CCAGNGTCAC ATATGTGGCG 240

GGGGGGTNGT GTCAGNNACA GNGTTTCCCC CNCCNGTNTT TCCCCCTNCC CCCCCCNCAG 300

GGGNAGACAA NGTNNTAGAG AGAACAGGGG TTATCCACAC ATCNCACTGN GNGGCACAGG 360

AGGANNANAN TTGTGCTNAG AGCCCCTGCN CTTCTGGTGG TANCTCTGGG GCCCATATTC 420

TCTNCTCTGG GTCCCCCCCG GGGGGGTGTN NCCCTCNCCG GGAGAGAGTN TTAGAGANAA 480

ATCTCCATCN CANATGANAA AATNTGNGGG NGAGAANCCC GGGGGATATC ACTNTTTTAN 540

AANNGACCCC ACCCCCCCCC CCCT 564

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 822 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GATTTGCNCT CATATNTCNT TTACCAAACA GNGGGNGTCT GCCCCCCTGT NATANACCTC 60

TTGTTNTCGC GGGGTGCTNN TNGGGGCCCC CCNTGTAGAA AAAGAACANN NGNTGTGGGN 120

GGGGGATTTC TCTCTGNTGT AGANCTNTNC NCTGAGACAC ACAGNGCCCT GTGTGGGGTC 180

CCCCTCNCCG AAAAAGANAC CCCNAAAAAA AAAAAAAAAN AGACCGCGNG GGGNNGAAAA 240

ATATCTCTNG NNATCTTCTC TCTAANCTCG CTTTTANTCC TCAGAAAACC CCACCCCNCC 300

NCTCTNCCCA GAAATATNAT ACANNNNGNG TTCCCCTNCC CAAAACCCCA AAGGGNNTCC 360

CCTCTCNTCT NCCCCNAATA CTCTTCCNCC CCTTNATTCT CNTATCTCTN NGGACTCANA 420

CTCTAAAACA CANGNNNCTT NTCTGTGCCG CAATNTNTTN TGTNACANGG CNCCCTGAAA 480

AAAACCCCCG TGTTCTCCAC ATCNCCTCTN TNATATCTCT GCCCCCTTCC NCTATATCNC 540

TGNGTTTATA ATTTCCAAGG AGAATGTNCN CAGGGGGGCC CCAATCTCCC CCCCTNGTTT 600

CNNCGAGNAG GGCTCTTTTN TATATTTTTN NTCNAAACCN CCNTTGTCCT TTTAAATNGG 660

CNTTNACNCC CNGNCCCNCC CAACNNCCCG ANCGGGGGAA ACGTTCCCCA NTTTTCCNTT 720

TCCCCCCGCC CNCCCNNACC CCAATNCCCT TTTTTCGCGT TCCGGGGGCC CTGTTTCCCT 780

AANCCCGGAA TNAANTNCNT TNTTCAANCC CCCCCCTTTT TT 822

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 553 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

TTTGGGTGCG GTCTCCTCTG TGTTAGTGTA TCCCCCATAG GGGGGGTCTC ACAGGGAGCC 60

CTTCTCTTTT GGGGGGTTAT ACACAGGGGA CACACATGTG ATATAGAGAG AACACATGAG 120

AGTGGGAGAG TGGGGGGGTG GGTGGAAGTG AGAAACAGAG AGAGAGAGAC TTTATTTTTT 180

GTGGTGTAAA ATGTGTTGAA TCTCTGGTTT GATAAATTTT ACACATTGGG GTTTGTGTAG 240

ATCCCTGATC TCTCTCCTAT CCCCATTCTC TTTCAGAGAT GTGTCTCTGG ATTCTCAGAG 300

AGATTTTCTG GTCTCACATG TTTGGTCCCT TATGTTCTCA CTCTCTCTTC TTTATTCTCT 360

GATACATGTG CTCTTCCCCC TTGGGTCTTC TCTCTGTCTC TGTCTCCCCC CCCATGATAC 420

ATAGAGTGTG TTTTCTCCCC GGGGTTTCCC TTGTTCACAA GAAGAGCTCT GGGGAATCTC 480

TATCTTCTCA AGGGTATAGC CCCCCAGTCC CCAGGCCCTT TTTCTTGGAA TTTTGGAGGG 540

GGTTCCCCAT TTT 553

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 904 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGGATTTGCT CTCAGATGGT AGTTTACGTA AACTGTGGGT GTCTTGCCTC TCTCTCAAAA 60

CATGTGCGCG TTTCTGGGCC CGTGCGCGTT TTCTGTGCTC CTCCTTCTTC ACTTCTTTGT 120

CGCGGGGGCG CTCGCCCCTG TGTTTTCTGT GCTCCTCGGG GAGATGCTCT CCCTTGGGGC 180

TGTGGGGCTC TGTGGCGGTG GTGGCGGTGT CCTCGATACC GTGCTTTTTT GTTTTCTCGA 240

GATCTTACTT TTTCCTCTCC CCCTTGTGTG TTTCTTGGGT ATACACGAGA TTGTGTGTGT 300

CTCTTTTCTT ACCCCCTCTC TAGTTTATAT TCACACTTAC TCTCTCTCTT TTCTTTTTCT 360

CTTTAGATTC TATCCTTTGT GCACTTTTTC TATTGTGCTC TAGATTTCTC CCCTTTTTGT 420

TTATTTCTCT TCTCCCTGTG TCCAGTGTGG TGAAAAAGAC CCTTATTAAA TTTAGACTTG 480

TGCGCTCTCT TCTTAAATTT CATGTGTTCT ACAGTCTCTC TGCGCTTTAG ATATTTTTAG 540

AAGCGCCTAA ATCTTTTAAA AT GTGTGAG ATCTCTTTTT TTTTTTTACA CTCCTTTGTT 600

TTTTCTTACT CCTCAGGGGC ATATAAACCC CCCTCTCCTT TAATATTTCT CACTCTCTTT 660

CTTTTCAAAA AAATTTTTCA ATCTAAATCC AAATTTTTTT TTTTTTTTGG TGGCCCCTAA 720

TTTTTGGGAA CGGCCCCCCC CCCTCCTCTG GGCCCTCATT GGGGGGATTT TTTTAATTCC 780

CGTAAATAAA AAGGGTCGGG CCCTTCTCCC CCCGTGGGGT AATTAATCAA GGATTTTAGG 840

GTTGGTAAAA ATTTCGGGTT TTGATGGTTT TGCCCCCCCC TTAACCCCTC TTTTTTTTTT 900

TTTT 904

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 698 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CTCAGCACTG AAAGAGATAG ATTAAAAACA AAACAAAACA ACAACCAAAA AAATACAAAC 60

AAACAAACAA AAAAAAACCC CAAACAAGTC GCTCAACTGT CTTGAGTCAA TAGATTTTAA 120

AAAATGAGTT AAGGTTAGGG TTAGGTTAGG GTTAGGGTAT AGCTCAGGCA GTAAGGTACT 180

TGCCAAGAAT GTTTGAGGAC CTAAGTTTGN CTTTTTTCTT TCTTTCTTNT GAAACAGGGT 240

TTCTCTGTGT AGCCTTTGNT ATAGACCAAG GCTGGCTTCG AACTCAGAGG ATCCACCTGC 300

CTCTGNCTCC GAGTGNCAGA ATTAAAGGCA TGTGCCATCA CTGTCCAGCT CTTAGGTATT 360

CATTTTTCAG CTTATAGTCT TTTGGCAAGG GATGCCAGGG NAGGAACCAG AGGCAGGGTT 420

GAAAAACAGG CCACNGNGGG GGGAACGCTG CTTCCCCGGG TTATTTTCTT GGGTCANATC 480

NTGTGGCCTT CCNGGGGGGT CTTTCCCCTT TCAAAATTNT TTGGGNTTGG GGNGGGGTCC 540

AAATNANTTT TTTNGGCCGG GTTTNGGGGN CCCCCCNNTT TGGNTTTTTT TTTAGAAGGC 600

CCGGNGGGGA NAAACCCCCC GGACTAAAAA AAAAAGGGGG GGANCCCCCC NGGGGNGGAA 660

TTTTTCCCGN CCCTNAAAAG NAAAAATTTT TNTTTTCC 698

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 851 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GAAANAANTC GGGAGAAAAA NAAANNNCCN TTAAGAGCTT GCCCCCANAG AAAAANTANN 60

AANTNAAAAA CTGNTAGACC ANNNGAAAAG GAAGCGCAGT NANAAAATGG TTCCTACGGG 120

TTAANTAAGA AGCANGACNG AAAGANNGNN TNNATNTAAC CGGGGNTAGN AAACGGCCCN 180

CTTGTANNAG GACCNAATCG AANTAGTACG ATCATGNTAC ANAGGGAAGG GGACGTTACC 240

CNCGGANGAA ACCCGGCACA AGATCTCNNA AGGGAGAAGA TTCTGAACGN NANNAANCCA 300

CAAGGAAATT ACTGTGGANA CGGGAGGAAT CNATNGTNAT NNAGNNNAGC TGGNCACTTT 360

GANAAGGCAT CGATANAANT GATGATGGNT CAGGCGAAAG AGCATACGTA AAACCAAGCA 420

AGGNGGAATA GTCATANAAC CATGNAAAAA ACNTTCAATA AAAGATNNCC NGAATATTGA 480

TCNGTANNNA ANAACNCCCG GTGGCCGTGA TTCCTTTTTT AACGGCAAAC AGCANNTTAG 540

TTTCAGATCA CCCAGATCAT CGNTGNAGAT NCCATNGATG TTNTTGAAAC TNANCTNGAG 600

GATTCAAGAA NNGNTGACAT GGTGAAATGA TGTACAAATN ACAACANAGA NCGTCGAGAT 660

NNTATTCCCC CNGNATGNAN GGACNTCTTA TGATGAANAC CTTATACCAG ACTCAAGTAN 720

AACNATATGA TCCCATGAGG GNGGNNACCC AGGNAGTCAN GAANAAATAC CNGAGAGTTA 780

AATGCNTTTT TTTGTNTGNG AACCCANTGC CCGACCTNTC AAANAGAAGC ANAGCCCNAA 840

AATTAATCCA A 851

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 936 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CTAAGGAAAA GGTTTTAGGA GGGAAAACCA ATAGGCCCTT GAGTTCTTAT TCTTAAGACA 60

TTGTAAAGGA AAGGTTTAGG GGAAAAATTA CCAGCCCGAT CCATTAGGGT TCCAAAAGAA 120

CCGTTCTTCC ATAAAGGCCA GAGTTCACCA TGAGTAACCA GGATGTTTCT TCGGACCTTA 180

TAAATATATT TTGAGGGGTT CATGGAATTG GGTTGCCATT TGGTAGTTGG TAGCCTACCC 240

TGCTCCTTCC CAGTGTTGGA TGCAGATATG CGCCCTGTTG GTTTTGAGTA GTTTTGAGAT 300

CAGTCAATTT TAGGTTTTAT GGCAAGCATT TATTCATCCC CACATTTTCT GCCAGGGTGT 360

AGTAAGTGAG TTCTTACAGA GCAGAGAGAA GGAGCAATCT GTGTTATCAA ATCAACTAGC 420

ACCAAGCACA CCAAGCAGCC AATCCTTAGA AGGAAGAAGC AAACACTTGG GTATCCTTCC 480

ATGGCTAGGA AATCTTCATG GCTCACGAAC CTTGGGATTT CCCTGTCAGG GTAGAATACA 540

AGCAGCTGAG ACCGAACAGG TATGGGTGGC ATGTCGAGAC AGGAAAAGAA CCTGTGTCTG 600

GGGAGAGGTG TGTGCTACAA AGCCAGAGAG AGGAACAGAT AGGGAGGGGT GTGCTGCACC 660

ATCATGGAGG GGGACAGACG ATTTGTCCCC AAGGAAAAGC TCCCTTTATG AGAGTTCTTA 720

CTGAATTTGG GAATGACATG GGAGACCAAG GGCCAAAGTC CAGATGAGCA GAGTGGGGAG 780

GAGGGTTGGA AAGTTCCAAG GAGAGAGGCG TGGGGGTAAG GGAAGCTCGC AGGGCTCCGC 840

CTCTGCCAGT GACCTTGGAC CGCTTTCTCT GAGGATCAGA GTTATCTGTA GGGGAGATGA 900

GGTTGAAAGA TACCCACAAT AACTTTGGCA AGTAGA 936

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 911 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GGGAATTTAA GGGNGATTTG GAGACTTTNG AATTTTCGAA NGTTCCAAAA TAGANNTTNA 60

GGNCAATGGG NTTGGGGCAG NGGNGCTTTT TTAAATCANA NAAGTATTAG ATTTNTATGG 120

AAACCCTGGG GGTTCCAGTT TAATCCCTTC ATCATCTTGA AATATNACTT GTTTATGGGA 180

ANGGTGNGAT AGCAGCCNGA AACAGAGGTT TTTATTATTA CTGTTAGAGA NGAGGATTGG 240

GGAATAGAAC AATGAGAGTC TTGGTAATAT TNTTCNGGAA ACAACNGACA TAATTGGAAC 300

ATTAAGGAAA TATATCCATG CATTCTGTAC TTGCAAATTG CTCCAAGGAA GATGGAGAGT 360

ATTGTATTTC AGATAGAGAT ANGACTATAC CTGTTATTTT TTTCATTATA GCAACATTAA 420

AAAAGATAGT AATCTAATTT CACATAACCA TTACTACTAA AGTATATATG TANTCTTTGT 480

TTATCAGGTT TTACTTCTCA GAAATTGCAG CATCTCCTAC AGAGCCTGTC AAATGAGACN 540

GCATAGATCC CCAGAGAACA GAGAGACTGG GAAATCATTG AAATTACACA ATCCTATCCC 600

AAATGTTTGC GTAGACTCAA GCTCGTATCA GCTCATAAGA TCAGTGTGTG TGTGTGTTTG 660

TGTGTGTGTG TGTCCCGCAC ATGCTTGAGT ATGCATGTGT GCATGCATGT GTGTATGTCT 720

ATTGCATTAG TAGAGATGTT AAGGTTGAAT GTATTTTCTG CTCATGGTCA TTGTAAGATA 780

TTGTGCTGTA TGTGATAAGA ATCAATGTAA CAAGGCTGGA GAGATGACTT CAGCTGTTAA 840

AGGCTAGACT CACTACCAAA AATAGNGCNA TCAGTGTGAA NTTCCCCACA GGAGCTTAGC 900

AAGNTAATAG G 911

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 781 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

TTCAGGGGTA ATCCTAAGGT AAACGGACAA AGTAAAGGGG AGGTTGGACC AATAAAGGGG 60

AAAAATAAAA GATTAACCGG ATGTTCCCTG GAACGACAAA TTGCCTTGGA AGTTTCCTAT 120

ACGGAAAAAA ATGAACAAGT TTCCTGTAAA GCAGGTAGCC GGAACGTTTC TAGGCTATAA 180

ATTTAACTGG CCTTATATTT ACAAAGTCTA AACATTTTAC TGGGGCATTA CAATTTTATA 240

ACACTAATTA GATCATGTGT GTACACCCAC AGTCTGACAG ACAGGGTATT TTTTCCTTCT 300

TATCCCAAGT GAGTTTAACC TTCCTTCTCC ACATTTATTG CCATGTGCAA TGCGTAGCTT 360

CTATTAACTC CTGATTATTG ATTGAACTTT ATGAGACATA AGAATGTACT TGACAACAGC 420

ATGTGAGAAA GGGAAAGTTG AGGGACTGAG TGTAATAGAG ACTGATAAGA AATGAATGGG 480

CTGTGTCTGA CTCTTATCCA ACATTCCAAT TCTTCAAGTC TAAAGGTGAA GGGTCATTTT 540

CAATCTACTA AGTTTGAATA TGATTTGTGC TCCTGGTGTC TACAGAGTAT TAGGAAATGT 600

TTGGTTTGTT AGGTCATTAG GGTAGGGCTC TTATGATAGA ATTCTTGTGG CTTTACATGG 660

AAAGGCAGAG AGAATACACC CACCCTAAAC ATTTCTGCCA TTGTGCAATA CAGTAAGGTA 720

TATTTCTTTC TTTTTATTAA CTATTTGGTG ATAGTGACAA ACAACTAGAC TTCATATGTG 780

A 781

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 389 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TTGCTCTTAG GAGTTTCCTA ATACATCCCA AACTCAAATA TATAAAGCAT TTGACTTGTT 60

CTATGCCCTA GGGGGCGGGG GGAAGCTAAG CCAGCTTTTT TTAACATTTA AAATGTTAAT 120

TCCATTTTAA ATGCACAGAT GTTTTTATTT CATAAGGGTT TCAATGTGCA TGAATGCTGC 180

AATATTCCTG TTACCAAAGC TAGTATAAAT AAAAATAGAT AAACGTGGAA ATTACTTAGA 240

GTTTCTGTCA TTAACGTTTC CTTCCTCAGT TGACAACATA AATGCGCTGC TGAGAAGCCA 300

GTTTGCATCT GTCAGGATCA ATTTCCCATT ATGCCAGTCA TATTAATTAC TAGTCAATTA 360

GTTGATTTTT ATTTTTGACA TATACATGT 389

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

AAATCGGGNT TNCGCGATTC GGTAATGACG NCNNATCCGT AAANNCATNC GCCGNNATNC 60

NATTNGAAAA TNCCGGGNGC AANNCGATGT CTNATTGAGG TNNCAGANCC ATCCGGCACA 120

GGCAATANGN AAAAAANGGG AGTTTCACAA TGTNTNTGAA TNTGNANCCA TTGGGCCCNA 180

AAAANTCCTN CGNTNNATGA ACCTTNNCGT NCAAAANTTT GGTNCGACNC AGCNGCTTTG 240

CNAGCNTTNA ATAAACACCG GNNTCCANAA TGNNACCAGN GNTGTTTNTN TCNANTNGCA 300

TNNCNNTTTG GAANCCCNCT TTTCCCAAAA CNTTNAAAAA 340

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 557 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

AGTCCGGGNA TGGTGGCANA TGCTTTTCAT NCCAGCACTT GGGAAGGCAA AAAACAGTTA 60

NACCTNAGGT TTANCCCAGN CTTTATTAGN ACCCCGTGTT CTNAAACACA AACNACAAAA 120

NTTTGNGGGN NTTTAAGTGN AAACACTGTG TAAAACCTTG GCCCTGATGN AGGGNTCTCC 180

TTTNGAACAG AAAATGTTTG AAGANTCCNA AAACATGTTG GGATGCCANA CGNGTTNTTG 240

NGCATCCATC TCAACGANGT TTTGNGAATA AATGGCAGGT NAAACTAGTA CATCATCATG 300

TNGNANCCAC CGGGCNTGCA GATTTGTGGT GGGAACCAAG TCCTCCCATA AAACAGGCTC 360

CTGTGGTACN AACAGGGCTG GANCCACNGA ATCAGTGCAG NTCTGGACAC CTGTCTGGCC 420

GGANGGNCTG GNCTAAGTNA ANNCAGGGGG GGCAAGAGCA TNGGANCNAA CGNCAGAAAN 480

CGNCCCNCCC GGTGAGCTNT TCCATGCCTN NCCTCGNTTT ATTTGGCACT GGGCATGTCC 540

CAACTNAACT TAGGATG 557

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 302 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GCCTATAAGT TTTGATTCCA TTCGTGAAAA TTTTTCCTAT ATCCCGAANA GTCCACTTAT 60

TACTACTGCG GCCTATTTGG AAACTAACCG AAATTCAGTT AGTTCCCTAG TAGCCTGCTC 120

TTGTAATATG TGTACTTTTC AATATTATAA AAAATTGGTC AGCAGATCTG AGTAAAACAG 180

GTGAAATTCC GATCGGTAGT CCAATTTGGT TAAAGAACAG GATATCCAGT GGTCCAAGGC 240

TCCAGTTTTG AACTCAAACA ATTATCAACC AGCTGNAAGC CCTATAGNAG TACGNAGCCC 300

AT 302

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 820 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GACTGCCTTT TTTTTCTTCC CAAGGATACC CTGCAGCACC CAACAGTAAA AGACTTCATA 60

AATAGGCAGC TTGGAGAAGA AGGCATTACC ACTGAAGCCA TATTAAATTT CTTCCCTAAC 120

GGTCCCCGAG AGAACCAAGC TGATGACATG ACCAGCTTTG ACTGGAGGGA TATATTCAAC 180

ATCACTGACC GCTTCTGCGC CTGGCTAATC AATACCTGGA GGTAAGAGGC AGCAATCCAC 240

CCGAGGACCA TAGTGAACCT CTTAATGTCA TGGGTGAGGC TAGAGACCTG TTAGCCAGTC 300

AGCTGGCACT GGATTCAGTC TTTCATCCTT CGCACAAAGT GGTAAGGGTG CCATGGCCAT 360

CTGACAGACT TGCGTGCGAC TGTCCTCACA TCTCGATAAC TTCATGACTC CTCTGGCTCC 420

CCCTCTTTCC CTTCCAGCAC ACATCCATTC CCAGCTATCT CCGGGCTGCC ATTGTCTAAT 480

GACTTCTGTT GGCCGGTGTC CGCCAAACCT TTGAGTTGAG CTCATTGATT GTGGACACTT 540

TACTCAAAGT TTAACAGCAT GTGAAAGACC CCGCTGACGG GTAGNAATCA CTCAGAGGAN 600

CCTCCAAGGA ACAGCGGGCC ACAAGNGGTN AACTNAANAG GGTTATTGNT AACGGGNNCC 660

GGGANCNAGT AATCGGGNCT GGCCCCAANT AAGGGTTTGG GCTTTATTNN CNGGGACAAA 720

AACCGCAAAA AAANNAAACG CCTTNTTGTA TTAAAANGCA NGNTTTTAGC CTTGGCCTGA 780

AATGGNGNTA AGNTACGGCC CNCNGTCAAT TCCTACTATA 820

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 955 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

AANCCGANAN TTTNAAAAAA CAANNANAAN GGGCCANGAN NTNAATANTT TCTNAAAAAA 60

NGANTACANG NACACGGCAG GGNNGTTTAG TCAGAATANA ATNNAGNGNN AACCATTGNC 120

TTTTGAGCAG GGTTTATNGG NCTACGTTGA CCCAAGTCAC ANTGNTANCA GAGATNANNG 180

AGGGGGNGGG AAGGGGTTNG GNTTTCCACA GCNTTNAAGT CAGAANTNGG AGAGACATTT 240

NGCCNTGATT CANGNCTTTN CCTCCTTATT TCCNANCNTC NCATTAANAN NAGAAAAGAG 300

TNTTTTNTTG TNTTGNGNAC AGGTGCACAA GTTTAGNANA GAGGAGACAN TGTNTAGAGA 360

TCAGATACGG ATGAGAGTTT CCGGGGANAG TATGNGGGGA TTTTCAGTCA GNNCACTACC 420

CAGAANGGAT TCAGTCGNGA GGAGNCAGGG ANGGGGTGNT GGAGTTNAGA CCGANAGAGC 480

GGNTAGCATN TAATGNNNAG AGAACACACA TNTTTTGGAT TTNAGAGACG NCCAAANCGC 540

TATACANGAT NTNTCGNTAN AGGGTGAAGA GTGAAGAAAG TGATGTCTCC ANCGCANACN 600

GGAACANGCN GCGANTTTCT TAGAGACCNA GGTTTTGATA NAGGGAAAGT CTATTCAAGC 660

CTCCCGTANA CTTGTAGGNC AAGNAAATAN TGCNNATTAT GAGNCCGTTG TTNTCAAACC 720

ANGTCCCCTA TAGCAGCAAA NAGTTGNCAG AAANTCNCAC AGAGNTCCCC CGTGAGATNG 780

NNNTTATNGN GGACACGATG TCATCAAGAG GGAGTNNTGN ACTGTGACTC CAGTCCTGTT 840

GAAGNGCATA GTAGACCATT CGCCGTGTTC ACCNACANTC AGCCNCTACC AGCNGAAAGA 900

GNAAAGGAGA GAGTTCGCAT ATGANAGACC CCACGGGTAG TTTGCAAGTA ATGAG 955

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 886 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

NTNGAAGNAN AAATTNGNAA AAANNCCNAA AACCTCCAAA TTTGCTACCA NTCTTCNACG 60

GTNGACTTTT AAACAAAAGG AGGGGGGGGT TCTTNTTCAA ATGGGCCCCT TCCCAATCCT 120

GTTCCCNAGG CAATTGTTTC TTNTTTCANC NTTCAACGGT TTTTGGGTTC CATCCAACTT 180

TTATTTNACC CNTTGAGTTT CCTGGCCGGN GCCTAGGGAC CTCCTTTTTA CNTGGGCCAG 240

TTCCCGTTCA AGACNACCCG GCGGTTAGTG GNCATGGGGA GATGGCCCCA TGANTCCAAG 300

ACAACTGTAT TCCCGGTTTT TTAGTATTTC CAAGCTTCCC GCCAATTTTT CTTCCTTCCG 360

CTTCCAGACA GTTTTGCCAG TNACGTGATT CGGTTCCGAG GCCCCAGCAC CATGGAGANT 420

GCGCGCTGTA NTCTTAGAAG GGCATTCTTC CGCCCCACNT CCCGGTNTAG CCNGAAGGCC 480

CACGGAGCAA CGAGGAGAGC GACGNTNTCT CCACAGCCGT GGCTTTTTTA TGGTTGGCAC 540

TTAAGGNTTC GCCGCCATTT TGTCCGTTCN TNGAGTTATT GTGTTGAGGG CAAGATCTTA 600

CGATTGGGTT TTGAAGGCAT GGGTAGTGGC TTGTAGACGC ATGGCAGGAG TTGGGATTCG 660

TTTGGGGACA CTGAGGGGAA GCCGNTTCTT GGGGTGTGTC CCCTNGACGC TGTTGTGGGT 720

GGGGACCGGA ACTAGACGTG CCGGGCTGCG GCGCCCAGCG TGGGAGGACT CGCGCGGGCT 780

GGCAGCCGGG CTGGGTGTCC CGGCGCCTCA CTCACATTTT TTGCCACGAT TGTCGCCTGG 840

TTTGATTTCC CACCAATCCC CCAGACCGTG CACGAGGAGT AGAAGC 886

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 900 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GGGNGTTNGC TCTCAGATGC NAGNTACNNN TCAGGGGGNG TCTCACGAGA AAANCTNATG 60

TGTGGGGGNT ANTNTGTATC CCCTNNNCTC NCTCGAGANC CCNNNTCTCG ANATTTTGGN 120

GACCNGGGGC CGGGGCCCAG ANACTCNCCA CCCCATATGG NGACCCTNTA TAAGTGTCNN 180

CCAGGGNNTG TTTTGGGNAA AATATANCNN ANAGNGGTGT NTNTNANATC TCGGGGGGTG 240

ACAGACCCNN ATTTTTTTTT ATAAAGACCC GGGGCATNTT CTCNGCCCCN TCTCCTCNGC 300

TACANGNNAC CCACACACAG TGTGTCTCCT CTCAGCCCCC TGGCACACTT TNTNTNGANT 360

CNGNGGGGAT ATGAGATTCN CNAGACTGGG NCCGCNNTAN TANNCNCCCC CNTGTCTCCT 420

CTCATAGTGT NGTGTCCCCC CCTCACCCNN TNTTGNGGTN CCCTACACCC ACACAATNTA 480

GACTCTNCCC NCCNTCNGCT NTGNGACNCA CANCTGNAAA TCCCGNNNCN CAAAAAGGGC 540

TGTNCTCCTC TCTNTTACNG GGNGGTCNCC CNCNNNNGAC TCTNAAANGT CCCTCNCAAA 600

AGGGACNCTT TTCTATACAC NCTTANTTTN CCTCCTTTGT NTNGCAAAAA ANNANCCTGT 660

GTTNCCCCCC NCTTTATNAT NTTTNTTTTN TTCCCCAAAC TAANCTTTTA GGNNTNANCT 720

TCCGGGGCCC CAACCCCAAA ATCCCANTNT TCTTTTNTNT TGGTTGGGGT GTCAAAATTC 780

CTNCCCCTAA ANTTTTGAAC CCCCTTTAAT TCCCCCCCCC GGNTNAAGGC CCNACTTCCC 840

TNGGNTNTTT TCNCTAAAAA ATTTTTTGTN GCCCTCCCTG GGAAATCCCC GGTATTCCTC 900

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1033 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CCTACGTTCA CCTATGCGTA ACAGATCTGC TGTGTCAGGA GCCTCCTACC CTCGCGCATC 60

CTGACCCCCA ACCACGTCCT CTTATCTGAT GACTGGTCAT CTTCCCAAGT CATACACCTC 120

ACCAGATCAC TCGTGGGGAT CTCTAGGCCA CCTCCTGTGG TACCCTAGGC CTTGGATCAC 180

TACTAACTCC TGCATCGTGG TAACCTCAAT GGCTGATCTT GAGGATGCAG TCTGGAGTTC 240

GACTCCATCA GGAAGCCACA TGGGGAGGTG GCTGAATGCC ACAGGCACCT ACCACATAAT 300

GCTTCATGTC CCCACAATAG TGTCATCAAG CANCGNTATC TCCCTTTGTA CCTGNCTATC 360

ACAGTAGGCC CTATGTGTTG AAGACAGAAA CGTTCTNATA CTCAAAATAG CTACCTACTT 420

TCATCTTTAG NAAAGTTATC ACCAGAGATT TCATCACATG NCTNGGCTTA NGTATTTTAT 480

CCCCTTTCTG AACTATTTAT CACGGGCAGA AAATNTACTG ATTATCCCTG TATCATGACA 540

TCGTGCTGNA GAGAAGACCC GAGTGGGCAG CATGGNGATC CAAGGAGACA AGGGAAACCA 600

AGCAGCTATA CATAGGATGT CAGCAGCAAG CCCTTCCCTG CCCACGTCAG ACTAAACCCT 660

TCAGTCCCTT CATCTTTTCC TAGAAGGGTT TGTAATTTCT GTTGATTGTG CACCAGCGCT 720

TCCCAATCGC TGAACATCTT TCTTCGAATG TGACTCAAAG TGAGTGCACC GAGTCTGGCT 780

AATGTCCTCT GCTCCTCTTA ACCTCTGTGG CACACTCCTC CTAACACATG TGTGTCGTCT 840

TGTTCCACAG TGGCCCCACG GTACTGGTTT CAATATAGCT TATGTATGAG CAATAAGGGC 900

TATGTATTTT TTTTTTTCAG ACACTGTTCC TTTTGTATTC AACAACCTCC TCACATACTC 960

AGCCGNACCA CATTTCTTCC AGGTCAAAAA CCATCTCTCC AATTTGTTAT GAATTACTCC 1020

TNCAAGTTCA GGT

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 883 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GGGGGGNNAA NAATTTCCCA AAAANNGNNG GNCCCNTTTT TTATCCAGTT TNNGGTTGAA 60

NATCTCNCCC CGGTTTNAAA ACCCNCAATG GGGAAAAAGG TACANCNGAT TNTTTATNGG 120

TTTGGGCGGA GGGGGAAATT TTTTTGGTTT TTTTNTTTNN GGGATTTTTG AAAAAAAAAN 180

GAANTTTTTA GGTTTCCCNN ANGTAATTTA TTTCAATGGA CCATTTTTGG GGTTCTCCCT 240

TTTGTAANAN GTTAAAAANA AGGGANTTCC AANNTTNCTT TTCAGTTTCC AGTTTCACCT 300

TCNGTAGCAG ACCCAGTTTT CATTTTGAGN TGGTNCCNAA AAGGNTTCCC AACTATGTTC 360

AATACCACAG GCAGCCTGCA GGAGGGAGAA TGGGTATGTA TTTAACAGCA TTTGACCAAA 420

TTATAAGAGC AGAGAGGAGC TTTACCAGGG ACAGGAAGGC AAAAGAGCTG AATNTTAAAC 480

AAAAGAATAA GAACAGGATN TCATCTGTGA GCTGTCACAG TGGGTTTGCA GAGCAGGAGA 540

ACACAGACAG GATTAGCTAT AAAGTTGTTA CATTAGTTAT TNTATTGGAG CATACAATAC 600

TTAAATAGTT CTAGGGCAAG AGAAATGAAC AGAAATGACC TTATAAGAGC CAGAGCTGTA 660

GCCACAGCTT TCTTTGTGCT TAGTTTGNTA GTTCANTCTT TCCAGGGCAG TCTGGTGGAT 720

NACACCAAAT TGCTTTAGAA AATGCTAGNT CTACTGTCCC TGTCTATTGT CAGCTTTGCA 780

ATGTGCATAG TGACAGGAGT TGCCTGGGAG CTTGGGGCTT ATGTTTTGCA GATCCATTGT 840

AATTAAAAAA GAATTGTAAG GAGATGGAGG CACGGGGTGA GGG 883

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 892 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GGGCCCCCCT CGAGGTCGAC GGTATCGATA AGCTTGATAT CGAATTCAGC TCTTAGCAAT 60

CTGACACCCT CTTCTGGCCT CTTCAGGCAC CTGCATGGTT CCACAGGACT GTCACACCCA 120

CGTACATAGA TAGTCAAAAT CTAGAGCACT GTTTCTATAC CTGTGAGTTG CAACCCCTTT 180

GGGAGTGCGG TCAAATGACC CTATCACAGG GGTCTCAAAT GAGATATCCT GCATATCAAA 240

TATTTACATT ATGATTCATA GTAGTACCAG AATTACAGTT ATGAAGTTAC AAAATAATTT 300

TATAGCTGAG AGTCACCACA ACATGCATAA CTGTATTAAA ATGTTACAGC ATTAGCAAGG 360

TTGAGAAATA CTGGTCTAGA GCCATTCCTT GTGCTGATAA AGGTGGCAGT GAGCATTATC 420

TTTCTGTCTC CACACCACTA GCAAATTTTT TCTCTATATA TAAACATGTA ATATGAGACA 480

GTCTGAATCC ACTGAGGCAC GGTCTGACTC CAGAACAAAG GATCGTATTC CTGAAAAGCA 540

AAACGTGTGT TTGGCACTGA CTGTGTGNCC CAGGTTNTCT TTCTGNACTC CTAGAGGTCT 600

GTANTGGGTC TTGAAGCACA GATNCTCTAA CCTTACCCTG GNNGCTCAGT AGNATGCCCC 660

AAAACNCANG NTGTTCAACA TNGGGNNCCN CCCNGAAACA GNGNTGTNGG ATTTGGNAGA 720

AAGGTGNAAT NCTTTGGGCN NNTCGGTTTA GGAATTTTAA ACANNAACTG GCTTNCNAGG 780

TCCNTTCCGG AGTCATCCTT NCACTGGNGC CCNCTGGACC CGGNGNANNG GGCCANTTCG 840

CCAGTTCGTN CCCCTGGNAC CCNTCNCCGG GGGCNAAANG CCCCTNNNNT TC 892

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 884 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TGGGCCCCCC TCGAGGTCGA CGGTATCGAT AAGCTTGAGG GACCCACGTG ATGGAAAGGG 60

AGAAGCAATT TAGTGTCCTT TGTCCTCTGA CCTCCACAAG TGCTGTGGCA TGGGGACACA 120

GGACTGTACA CACACACACA CACACACACA CACACACACA CACACACGCA CGCACACACA 180

CCCCTCAAGT AACCGTGGAA TAAAGGTCCG ACCAGAAACC ACGCTGGAAC GGGAGATGCT 240

GGAGCACATC AGGGTGGTGC TAAGCAGCAG ATCGGCCTGT AACTGGCAGC AGAGGGGTGT 300

GGCTCTTTCA GAACCAGGAG GGCATCGCCC CTCCAGCCAG ACTCTCCAGC TTTCTTCCCC 360

TCCTTGCCTC CTGTTTTCCT TCTGCCTACC TTCCTTTGGC CTCAAACCAT AATGTGCAAC 420

ACATTCAAAC TGTAGTAAGT GTTTTAATTT TCTACTAAAC AATAAAACCT TTAGATTTTC 480

ACTGGGCCAG TGCTGGTAAC AGCAGACTGG GTGGAGTATC ACAGAGGGTG TGGAGCAAGC 540

TGGCTACCCA GGGCTGGGCA CACTCAACAC TCTGGCATTC TGTGGAAGTT CTGGGCAGTA 600

AAAACAGAAG CATACGTCAC GCACAGGTTC CATAGTGTTA GGCATCTTAA TCTATCTAGA 660

ATACCTGGTG TTTAGTTTGT TTACAAAATT GATTGTTGTA CTTGGACAGT GGTGTTTTTT 720

TCCCAGGGCT TCCAGGATTT AGGGGTATAC CAGGCCCATT ACATTGGGTA AACGTGTGTG 780

TTAATTTTTT CTTTTTAAAC CTCCTTGGTT GACTACTTGT TTTCCTTTTT AATGGTCCCA 840

GTTCCCCTTG GGGGGTTTGT TTTGGAAAAA GGCTTTCCGG TTTC 884

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 326 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

AGCACACCAC AGAGAGGGGG TCTCCGTCCC CGAGAGGCAA AAGTCTCCCA CTGTGCTCCT 60

CTCCCCCCCT GGTGGGGGTT AAGAGATGGG GGCTCTGGGG GGTGATAGAA CCCCTGGCGG 120

GACACCCCCC CGCTCTCGTG GAGAGAGACA GAGGGGGGTG CCCCTGATAT CTCACTAGAG 180

GGGAGAGGTG AGAGGGCTCC ACAGTGTGGT GTGGTGGTGA GTGCTCTATC TCCAGGTGTC 240

TCACATATTT TCACAGCTCT TGACCACAGA GAGATCTTGT TGACTCTGTG CTCGCGGAAT 300

CTAATGTGCC CCACATCATA TACACA 326

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 557 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GGGGGGGTCT CACNNTANAN CACTCNGGNG TCTCCCATGT CTAGATCTCC CCCCNGCNCN 60

NGNGANGAGT GTGNGGAGAT CCCTCTCTGN TCTCTACACT CTAAAGGGTA NGCGGGGAGA 120

GAGAGAGAGC ACANTCTATA GANCACANAG CACACNCGCT CNANGTGCCC NANTNACANG 180

NNAGAGAGAN CCCCTCTCNC AGTATATNGG GGAGAGAGTN TGAGGGACNC TCCTCTTTTC 240

TCTCAACNCT GNGGGGGGAG NGNGAGTGTT CTCTCTGNGG GGNGGAGNGG NACACTCNGN 300

TCTNCGTNTG NGTGCNCNNG TNTTCTGGGG GTCACANAGA AATCNCCTNT CTCAACACAA 360

CAACAACAAC CCCCCGCACG NGCACACACC ACAACAACAA NGGGACANCG CGNGGGGGNT 420

NGNGCACACC CAGNGGAGAC ACTGTTTTCT GTTTNACACA CACACACACA CACACACACA 480

CNCNCCCCCC ACANAGTTTT TNGGAAAANC GCNGGGGGGG GNGGGNCTTT TTGCCNCAAG 540

CCTTTTTTNA NCNCCCA 557

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 376 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GTCTCCCCCA AAGGGGGGGT CTCACCCTCC CGGACACCAC ACATCTGTCT GTCTCTCTGA 60

TCTCTGACAC CCCACAGAGA TATATATAGG GACAACGCCG CTGTCCCCAT GATATAGAGA 120

GAAGCGAGAC AAACTCTCAG GTACACATGA CACATGATCC CCATGATCCC CGGCACACTC 180

TTCTAATATA GTTGAGAGAG TTGTGTCTCT CAAGTGTCTC TGGTATTTTC TAACCCCATG 240

TTTTCTCTCA CAATGTCACA CGGGGGAGCT CGGACGCGGT GCACATGGGG GAGAGTTCGT 300

GTCTATGACA CACTAGTCTT GCCCCCGAAC CACAGAGACC TCGACTCGGG TTTAGTCTCC 360

TCTGCCCCCC CAGCTC 376

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 533 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ATNNCCCAAN ATCANATGNG GAANNNCCCA CATTTTNTAT NTAGAAANGN GTTTTGTGTG 60

TGTGNGTNNA ATTTGAGNTT TCACAGAGNT NACATTCTCT GTGTCACAAN CCCTTTCTCT 120

CTACACTCCA CAGTGTGGTG NGAGATATAC TNTGANACAN ATGNGCTCTC TCCTCNCCCC 180

CCNNCATGTT NTNCCCCACA GTNTACNNCN NCNATATATN GNNCNCNGNA GANNGGTATG 240

NGNGNTGTNT TTNTTTAAAA AGATNTNANA NAGNGGGTAT GCGTGNGGGG TATGTNNANA 300

CATATATGTN NNAGAGGGTC TCTCTGNGGC CCNATGGAGG CANATCCCCC CCNCTCNGAG 360

NNATATAGAA AAGAGTNTTT NANGGTGTTT GTGGACACAG ATAAGGGGAG AGAGAGAGAG 420

AGAGANAGAG AGAGANAGAG AGAGAGAGAG AGAGAGANAN GGNGTNTTNG GNTTCNTCCC 480

CCCCNATATA CAGAAAAANC GGGGGGGGGT TAGGNGGNNG GGGGTTTNCT TTA 533

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 346 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTTCACACGA GATGTCGCGA CTCTCGCGAG ACTCTCAGCG CGGAGATATA GACCCACAAG 60

GGGAATCCCC CGGGTTTTTT GCCACAGGAG AGCGCGAGGA GAGAGATATT CTTATTATGG 120

CTATAGACAC CCCCGTGGGT GGGGGACATT TGTGGTGTTT CCACAGGGGG GGGGATGTAC 180

CCCGGATATC AGAGTATTCT CTAAAAAAGG TGAGAAGAGG TCTTCTCTTT TGAGAGTATG 240

GGGACACTCG AGGAGAGCTC TCTATCTATC TCTCACAGCG CCCCTGTGTG GGCGGATCCT 300

CCACACCAGA TGTTAGTGTG NAGATCTCCC CATCTTCTAT ATTGAA 346

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 461 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GAANACCCAA AATTGNGCTN GTGGGCAAAN NTTTTNCCGT TTCTTGTGCT TGNGCGGCNA 60

AGNNAAAAAT TCAAAACCAA NACCACANAA GCGCGTTATC CTGNCTNTCT GCCNTTNCCC 120

TGTCACACTG NGGCTGTACA GACATCNANC GCTTTCTAGA GAGACGNGAG AGTCAGGGGA 180

CTCTTTCCCC CANNCGCATT ATANCCACAT ATTAGNGTAN NANATTCAGC TGTGNTNCAC 240

TGGGNGTGTC TCCNTAGTGT GAAGCAACAC AGGGAAACTN TTCGCNCACA TGTCCTCTGG 300

TGTTCACAGA NATAAGNAGG CTCCTAGACC NNTATNACTG TGGGNAGAGN ATGTTACCTC 360

CCTATANNTC GGGGTCTATC TCTGTGAGAN AGAGNTTCCT TTCTCCCATN CCTACCTCAG 420

TGGGGTGNTA TNTACATCNC AGAGAGCAGA NAACTGTGAG C 461

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GGGGTNTCAC AGAGANAGGG CACANCTCTC CCNAGAANGG GNCNNCCCTC TTTTTNNGGN 60

GTAACACCTC TCNCCGTGTC TCTTTCTTTC TTTTTTNTTT TTTGGGGGGC TCTTTTTCGN 120

GGAGGNGGAG NNCGNCCGAG GGTCGGGCNN NNCNGNGGAN AGCTCTNTCN CANNGATATA 180

TCNCCNNANC CCCCCTGTNT CTTATAANNN ACATCTCTTC NTCNCAGGGT CACACCNAGA 240

NTCTCNTTTC TACAACAACC CCCACACGCN AAAGCTCCCC ACNNNGNGNG GGGGTCTCNC 300

AAGAANATCT CNGCGGAGAG GTGGNGGAGA GAGTGANATC TGNATNTCTG GNTTCCCCNC 360

ANTGCCC 367

What is claimed is:

1. An isolated nucleic acid comprising a nucleotide sequence set forth in SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82 or SEQ ID NO:83.

2. An allelic variant or homolog of the nucleic acid of claim 1.

3. An isolated nucleic acid encoding the protein encoded by the gene comprising the nucleotide sequence set forth in SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37,

SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82 or SEQ ID NO:83.

4. A host cell containing the nucleic acid of claim 1, 2 or 3.

5. A nucleic acid that selectively hybridizes under stringent conditions with the nucleic acid of claim 1, 2 or 3.

6. A nucleic acid having a region within an exon wherein the region has at least 50 % homology with the nucleic acid of claim 1, 2 or 3.

7. A nucleic acid having a region within an exon wherein the region has at least 60 % homology with the nucleic acid of claim 1, 2 or 3.

8. A nucleic acid having a region within an exon wherein the region has at least 70 % homology with the nucleic acid of claim 1, 2 or 3.

9. A nucleic acid having a region within an exon wherein the region has at least 80 % homology with the nucleic acid of claim 1, 2 or 3.

10. A nucleic acid having a region within an exon wherein the region has at least 90 % homology with the nucleic acid of claim 1, 2 or 3.

11. A nucleic acid having a region within an exon wherein the region has at least 95 % homology with the nucleic acid of claim 1, 2 3.

12. A protein encoded by the nucleic acid of claims 1, 2, 3, 5, 6, 7, 8, 9, 10 or 11.

13. A nucleic acid comprising a regulatory region of a gene comprising the nucleotide sequence set forth in SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82 or SEQ ID NO:83.

14. A construct comprising a regulatory region of claim 13, wherein the regulatory region is functionally linked to a reporter gene.

15. A method of identifying a cellular gene necessary for viral growth in a cell and nonessential for cellular survival, comprising

(a) transferring into a cell culture growing in serum-containing medium a vector encoding a selective marker gene lacking a functional promoter,

(b) selecting cells expressing the marker gene,

(c) removing serum from the culture medium,

(d) infecting the cell culture with the virus, and

(e) isolating from the surviving cells a cellular gene within which the marker gene is inserted, thereby identifying a gene necessary for viral growth in a cell and nonessential for cellular survival.

16. A method of reducing or inhibiting a viral infection in a subject, comprising administering to the subject an amount of a composition that inhibits expression or functioning of a gene product encoded by a gene comprising the nucleic acid set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74 or SEQ ID NO:75, or a homolog thereof, thereby treating the viral infection.

17. The method of claim 16, wherein the composition comprises an antibody that binds a protein encoded by the gene.

18. The method of claim 16, wherein the composition comprises an antibody that binds a receptor for a protein encoded by the gene.

19. The method of claim 16, wherein the composition comprises an antisense RNA that binds an RNA encoded by the gene.

20. The method of claim 16, wherein the composition comprises a nucleic acid functionally encoding an antisense RNA that binds an RNA encoded by the gene.

21. A method of reducing or inhibiting a viral infection in a subject comprising mutating *ex vivo* in a selected cell from the subject an endogenous gene comprising the nucleic acid set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74 or SEQ ID NO:75, or a homolog thereof, to a mutated gene incapable of producing a functional gene product of the gene or to a mutated gene producing a reduced amount of a functional gene product of the gene, and replacing the cell in the subject, thereby reducing viral infection of cells in the subject.

22. The method of claim 21, wherein the cell is a hematopoietic cell.

23. A method of reducing or inhibiting a viral infection in a subject comprising mutating *ex vivo* in a selected cell from the subject an endogenous gene comprising a nucleic acid isolated by the method of claim 15, to a mutated gene incapable of producing a functional gene product of the gene or to a mutated gene producing a reduced amount of a functional gene product of the gene, and replacing the cell in the subject, thereby reducing viral infection of cells in the subject.

24. The method of claim 23, wherein the virus is HIV.

25. The method of claim 23, wherein the cell is a hematopoietic cell.

26. A method of increasing viral infection resistance in a subject comprising mutating *ex vivo* in a selected cell from the subject an endogenous gene comprising a nucleic acid isolated by the method of claim 15, to a mutated gene incapable of producing a functional gene product of the gene or to a mutated gene producing a reduced amount of a functional gene product of the gene, and replacing the cell in the subject, thereby reducing viral infection of cells in the subject.

27. The method of claim 26, wherein the virus is HIV.

28. The method of claim 26, wherein the cell is a hematopoietic cell.

29. A method of screening a compound for effectiveness in treating a viral infection, comprising administering the compound to a cell containing a cellular gene functionally encoding a gene product necessary for reproduction of the virus in the cell but not necessary for survival of the cell and detecting the level of the gene product produced, a decrease or elimination of the gene product indicating a compound effective for treating the viral infection.

30. The method of claim 29, wherein the cellular gene comprises the nucleic acid set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74 or SEQ ID NO:75, or a homolog thereof.

31. The method of claim 29, wherein the cellular gene is a gene identified by the method of claim 15.

32. A method of screening a compound for reducing or inhibiting a viral infection, comprising administering the compound to a cell containing the construct of claim 14 and detecting the level of the reporter gene product produced, a decrease or elimination of the reporter gene product indicating a compound for reducing or inhibiting the viral infection.

33. A purified mammalian serum protein having a molecular weight of between about 50 kD and 100 kD which resists inactivation in low pH and resists inactivation by chloroform extraction, which inactivates when boiled and inactivates in low ionic strength solution, and which when removed from a cell culture comprising cells

persistently infected with reovirus selectively prevents survival of cells persistently infected with reovirus.

34. A method of selectively eliminating, from an animal cell culture capable of surviving for a first period of time in the absence of serum, cells persistently infected with a virus, comprising propagating the cell culture in the absence of serum for a second time period which a persistently infected cell cannot survive without serum, thereby selectively eliminating from the cell culture cells persistently infected with the virus.

35. The method of claim 34, wherein the second time period is from about three days to about ten days.

36. The method of claim 34, further comprising transferring the cell culture from a first container to a second container.

37. A method of selectively eliminating from a cell culture cells persistently infected with a virus, comprising propagating the cell culture in the absence of a functional form of the protein of claim 33.

38. A method of reducing or inhibiting a viral infection in a subject, comprising administering to the subject an amount of a composition that inhibits functioning of a serum protein having a molecular weight of between about 50 kD and 100 kD which resists inactivation in low pH and resists inactivation by chloroform extraction, which inactivates when boiled and inactivates in low ionic strength solution, and which, when removed from a cell culture comprising cells persistently infected with the virus, prevents survival of cells persistently infected with the virus, thereby reducing or inhibiting the viral infection.

39. The method of claim 38, wherein the composition comprises an antibody that binds the serum protein.

40. The method of claim 38, wherein the composition comprises an antisense RNA that binds an RNA encoded by the gene.

41. A method of identifying a cellular gene that can suppress a malignant phenotype in a cell, comprising

(a) transferring into a cell culture incapable of growing well in soft agar a vector encoding a selective marker gene lacking a functional promoter,

(b) selecting cells expressing the marker gene, and

(c) isolating from selected cells which are capable of growing in agar a cellular gene within which the marker gene is inserted, thereby identifying a gene that can suppress a malignant phenotype in a cell.

42. A method of identifying a cellular gene that can suppress a malignant phenotype in a cell, comprising

(a) transferring into a cell culture of non-transformed cells a vector encoding a selective marker gene lacking a functional promoter,

(b) selecting cells expressing the marker gene, and

(c) isolating from selected and transformed cells a cellular gene within which the marker gene is inserted, thereby identifying a gene that can suppress a malignant phenotype in a cell.

43. A method of screening for a compound for suppressing a malignant phenotype in a cell comprising administering the compound to a cell containing a cellular gene functionally encoding a gene product involved in establishment of a malignant phenotype in the cell and detecting the level of the gene product produced, a decrease or elimination of the gene product indicating a compound effective for suppressing the malignant phenotype.

44. A method of suppressing a malignant phenotype in a cell in a subject, comprising administering to the subject an amount of a composition that inhibits expression or functioning of a gene product encoded by a gene comprising the nucleic acid set forth in

SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82 or SEQ ID NO:83, or a homolog thereof, thereby suppressing a malignant phenotype.

45. The method of claim 44, wherein the composition comprises an antibody that binds a protein encoded by the gene.

46. The method of claim 44, wherein the composition comprises an antibody that binds a receptor for a protein encoded by the gene.

47. The method of claim 44, wherein the composition comprises an antisense RNA that binds an RNA encoded by the gene.

48. The method of claim 44, wherein the composition comprises a nucleic acid functionally encoding an antisense RNA that binds an RNA encoded by the gene.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/06067

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :C12N 15/11, 15/12, 15/06, 15/10
US CL :435/6, 23.1, 325

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6, 23.1, 325, 172.3

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WATSON, James D., et al, Recombinant DNA, Second Edition, New York, Scientific American Books, W.H. Freeman and Company, 1992, pages 99-133, see entire document.	1-11 and 15

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

*	Special categories of cited documents:
"A"	document defining the general state of the art which is not considered to be of particular relevance
"E"	earlier document published on or after the international filing date
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O"	document referring to an oral disclosure, use, exhibition or other means
"P"	document published prior to the international filing date but later than the priority date claimed
"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&"	document member of the same patent family

Date of the actual completion of the international search 30 JULY 1997	Date of mailing of the international search report 13 AUG 1997
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230	Authorized officer JAMES MARTINELL Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/06067

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☒ Claims Nos.: 12 and 31
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
1-11 and 15

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/06067

B. FIELDS SEARCHED
Electronic data bases consulted (Name of data base and where practicable terms used):

APS and CAS: promoter#, serum, virus, viral, vector#
IG Suite and MPSRCH on SEQ ID NOs: 6, 7, 8, 22, 40, 41, 46, 69, 73, 76, and their complements